

47

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
25 May 2001 (25.05.2001)

PCT

(10) International Publication Number
WO 01/36467 A2

(51) International Patent Classification⁷: C07K 14/00

(21) International Application Number: PCT/US00/31363

(22) International Filing Date:
16 November 2000 (16.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/443,060 18 November 1999 (18.11.1999) US
60/170,320 13 December 1999 (13.12.1999) US

(71) Applicant: SCHERING CORPORATION [US/US];
2000 Galloping Hill Road, Kenilworth, NJ 07033-0530 (US).

(72) Inventor: GORMAN, Daniel, M.; 6371 Central Avenue,
Newark, CA 94560 (US).

(74) Agent: SCHRAM, David, B.; Schering-Plough Corpora-
tion, Patent Dept., K-6-1 1990, 2000 Galloping Hill Road,
Kenilworth, NJ 07033-0530 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, HR, HU, ID, IL, IN, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LU, LV, MA, MD, MG, MK, MN, MX, MZ, NO, NZ, PL, PT, RO, RU, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UZ, VN, YU, ZA.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/36467 A2

(54) Title: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

(57) Abstract: Nucleic acids encoding mammalian, e.g., primate, receptors, purified receptor proteins and fragments thereof. Antibodies, both polyclonal and monoclonal, are also provided. Methods of using the compositions for both diagnostic and therapeutic utilities are described.

MAMMALIAN RECEPTOR PROTEINS;
RELATED REAGENTS AND METHODS

5 This filing claims priority to U.S. Patent Application
09/443,060, filed November 18, 1999, and U.S. Application
60/170,320, filed December 13, 1999, each of which is
incorporated herein by reference.

FIELD OF THE INVENTION

10 The present invention relates to compositions and methods
for affecting mammalian physiology, including immune system
function. In particular, it provides methods to regulate
development and/or the immune system. Diagnostic and
therapeutic uses of these materials are also disclosed.

15

BACKGROUND OF THE INVENTION

Recombinant DNA technology refers generally to techniques
of integrating genetic information from a donor source into
vectors for subsequent processing, such as through introduction
20 into a host, whereby the transferred genetic information is
copied and/or expressed in the new environment. Commonly, the
genetic information exists in the form of complementary DNA
(cDNA) derived from messenger RNA (mRNA) coding for a desired
protein product. The carrier is frequently a plasmid having the
25 capacity to incorporate cDNA for later replication in a host
and, in some cases, actually to control expression of the cDNA
and thereby direct synthesis of the encoded product in the host.
See, e.g., Sambrook, et al. (1989) Molecular Cloning: A
Laboratory Manual, (2d ed.) vols. 1-3, CSH Press, NY.

30 For some time, it has been known that the mammalian immune
response is based on a series of complex cellular interactions,
called the "immune network". Recent research has provided new
insights into the inner workings of this network. While it
remains clear that much of the immune response does, in fact,
35 revolve around the network-like interactions of lymphocytes,
macrophages, granulocytes, and other cells, immunologists now

generally hold the opinion that soluble proteins, known as lymphokines, cytokines, or monokines, play critical roles in controlling these cellular interactions. Thus, there is considerable interest in the isolation, characterization, and mechanisms of action of cell modulatory factors, an understanding of which will lead to significant advancements in the diagnosis and therapy of numerous medical abnormalities, e.g., immune system disorders.

Lymphokines apparently mediate cellular activities in a variety of ways. See, e.g., Paul (ed. 1996) Fundamental Immunology 3d ed., Raven Press, New York; and Thomson (ed. 1994) The Cytokine Handbook 2d ed., Academic Press, San Diego. They have been shown to support the proliferation, growth, and/or differentiation of pluripotential hematopoietic stem cells into vast numbers of progenitors comprising diverse cellular lineages which make up a complex immune system. Proper and balanced interactions between the cellular components are necessary for a healthy immune response. The different cellular lineages often respond in a different manner when lymphokines are administered in conjunction with other agents.

Cell lineages especially important to the immune response include two classes of lymphocytes: B-cells, which can produce and secrete immunoglobulins (proteins with the capability of recognizing and binding to foreign matter to effect its removal), and T-cells of various subsets that secrete lymphokines and induce or suppress the B-cells and various other cells (including other T-cells) making up the immune network. These lymphocytes interact with many other cell types.

Research to better understand and treat various immune disorders has been hampered by the general inability to maintain cells of the immune system in vitro. Immunologists have discovered that culturing many of these cells can be accomplished through the use of T-cell and other cell supernatants, which contain various growth factors, including many of the lymphokines.

Various growth and regulatory factors exist which modulate morphogenetic development. Many receptors for cytokines are

known. Often, there are at least two critical subunits in the functional receptor. See, e.g., Gonda and D'Andrea (1997) Blood 89:355-369; Presky, et al. (1996) Proc. Nat'l Acad. Sci. USA 93:14002-14007; Drachman and Kaushansky (1995) Curr. Opin. Hematol. 2:22-28; Theze (1994) Eur. Cytokine Netw. 5:353-368; and Lemmon and Schlessinger (1994) Trends Biochem. Sci. 19:459-463.

From the foregoing, it is evident that the discovery and development of new receptors, including ones similar to known receptors for lymphokines, should contribute to new therapies. In particular, the discovery and understanding of novel receptors for lymphokine-like molecules which enhance or potentiate the beneficial activities of other lymphokines would be highly advantageous. The present invention provides new receptors for ligands exhibiting similarity to cytokine like compositions and related compounds, and methods for their use.

SUMMARY OF THE INVENTION

The present invention is directed to novel receptors related to cytokine receptors, e.g., primate, cytokine receptor like molecular structures, designated DNAX Cytokine Receptor Subunits (DCRS), and their biological activities. In particular, it provides descriptions of subunits designated DCRS3 (referring to two embodiments designated DCRS3.1 and DCRS3.2) and DCRS4 (referring to three embodiments designated DCRS4.1, DCRS4.2, and DCRS4.3). It includes nucleic acids coding for the polypeptides themselves and methods for their production and use. The nucleic acids of the invention are characterized, in part, by their homology to cloned complementary DNA (cDNA) sequences enclosed herein.

The present invention provides a composition of matter selected from: a substantially pure or recombinant: DCRS3 polypeptide comprising: at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 2 or 25; a substantially pure or recombinant DCRS3 polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of

SEQ ID NO: 2 or 25; a natural sequence DCRS3 comprising mature
SEQ ID NO: 2 or 25; a fusion polypeptide comprising DCRS3
sequence; or DCRS4 polypeptide comprising: at least three
distinct nonoverlapping segments of at least four amino acids
5 identical to segments of SEQ ID NO: 5, 28, or 31; a
substantially pure or recombinant DCRS4 polypeptide comprising
at least two distinct nonoverlapping segments of at least five
amino acids identical to segments of SEQ ID NO: 5, 28, or 31; a
natural sequence DCRS4 comprising mature SEQ ID NO: 5, 28, or
10 31; or a fusion polypeptide comprising DCRS4 sequence. In
certain embodiments, the invention embraces such a substantially
pure or isolated antigenic DCRS3 or DRS4 polypeptide, wherein
the distinct nonoverlapping segments of identity: include one of
at least eight amino acids; include one of at least four amino
15 acids and a second of at least five amino acids; include at
least three segments of at least four, five, and six amino
acids, or include one of at least twelve amino acids. Other
embodiments include wherein the: DCRS3 polypeptide: comprises a
mature sequence of Table 1; is an unglycosylated form of DCRS3;
20 is from a primate, such as a human; comprises at least seventeen
amino acids of SEQ ID NO: 2 or 25; exhibits at least four
nonoverlapping segments of at least seven amino acids of SEQ ID
NO: 2 or 25; comprises a sequence of at least 3 amino acids on
each side across an exon boundary; is a natural allelic variant
25 of DCRS3; has a length at least about 30 amino acids; exhibits
at least two non-overlapping epitopes which are specific for a
primate DCRS3; is glycosylated; has a molecular weight of at
least 30 kD with natural glycosylation; is a synthetic
polypeptide; is attached to a solid substrate; is conjugated to
30 another chemical moiety; is a 5-fold or less substitution from
natural sequence; or is a deletion or insertion variant from a
natural sequence; or DCRS4 polypeptide: comprises a mature
sequence of Table 3; is an unglycosylated form of DCRS4; is from
a primate, such as a human; comprises at least seventeen amino
35 acids of SEQ ID NO: 5; exhibits at least four nonoverlapping
segments of at least seven amino acids of SEQ ID NO: 5, 28, or
31; comprises a sequence of at least 3 amino acids on each side

across an exon boundary; is a natural allelic variant of DCRS5; has a length at least about 30 amino acids; exhibits at least two non-overlapping epitopes which are specific for a primate DCRS5; is glycosylated; has a molecular weight of at least 30 kD with natural glycosylation; is a synthetic polypeptide; is attached to a solid substrate; is conjugated to another chemical moiety; is a 5-fold or less substitution from natural sequence; or is a deletion or insertion variant from a natural sequence. Still other embodiments include a composition comprising: a substantially pure DCRS3 and another cytokine receptor family member; a sterile DCRS3 polypeptide; the DCRS3 polypeptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a substantially pure DCRS4 and another cytokine receptor family member; a sterile DCRS4 polypeptide; the DCRS4 polypeptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration. Fusion polypeptide embodiments include those comprising: mature protein sequence of Table 1 or 3; a detection or purification tag, including a FLAG, His6, or Ig sequence; or sequence of another interferon receptor protein. Kit embodiments include those comprising such a polypeptide, and: a compartment comprising the protein or polypeptide; or instructions for use or disposal of reagents in the kit.

Binding compound embodiments include, e.g., a binding compound comprising an antigen binding site from an antibody, which specifically binds to a natural: DCRS3 polypeptide, wherein: the binding compound is in a container; the DCRS3 polypeptide is from a human; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of Table 1; is raised against a mature DCRS3; is raised to a purified human DCRS3; is immunoselected; is a polyclonal antibody; binds to a denatured DCRS3; exhibits a Kd to antigen of at least 30 μ M; is attached

to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label; or DCRS4 polypeptide, wherein: the binding compound is in a container; the DCRS4 polypeptide is from a human; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of Table 3; is raised against a mature DCRS4; is raised to a purified human DCRS4; is immunoselected; is a polyclonal antibody; binds to a denatured DCRS4; exhibits a K_d to antigen of at least 30 μM ; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label. Kits include those comprising the binding compound, and: a compartment comprising the binding compound; or instructions for use or disposal of reagents in the kit.

Methods are provided, e.g., of producing an antigen:antibody complex, comprising contacting under appropriate conditions: a primate DCRS3 polypeptide with a described antibody, thereby allowing the complex to form; or a primate DCRS4 polypeptide with a described antibody, thereby allowing the complex to form. This includes wherein: the complex is purified from other cytokine receptors; the complex is purified from other antibody; the contacting is with a sample comprising another cytokine; the contacting allows quantitative detection of the antigen; the contacting is with a sample comprising the antibody; or the contacting allows quantitative detection of the antibody.

Various related compositions are provided, e.g., a composition comprising: a sterile binding compound, as described, or the described binding compound and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration.

Nucleic acid embodiments include, e.g., an isolated or recombinant nucleic acid encoding the DCRS3 polypeptide, wherein the: DCRS3 is from a human; or the nucleic acid: encodes an

antigenic peptide sequence of Table 1; encodes a plurality of antigenic peptide sequences of Table 1; exhibits identity over at least thirteen nucleotides to a natural cDNA encoding the segment; is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a primate; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding the DCRS3; or is a PCR primer, PCR product, or mutagenesis primer; or an isolated or recombinant nucleic acid encoding the DCRS4 polypeptide, wherein the: DCRS4 is from a human; or the nucleic acid: encodes an antigenic peptide sequence of Table 3; encodes a plurality of antigenic peptide sequences of Table 3; exhibits identity over at least thirteen nucleotides to a natural cDNA encoding the segment; is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a primate; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding the DCRS4; or is a PCR primer, PCR product, or mutagenesis primer. Other embodiments of the invention include a cell or tissue comprising the described recombinant nucleic acid. Preferably, the cell is: a prokaryotic cell; a eukaryotic cell; a bacterial cell; a yeast cell; an insect cell; a mammalian cell; a mouse cell; a primate cell; or a human cell.

Kit embodiments include those comprising a described nucleic acid, and: a compartment comprising the nucleic acid; a compartment further comprising a primate DCRS3 or DCRS4 polypeptide; or instructions for use or disposal of reagents in the kit.

Alternative nucleic acid embodiments include a nucleic acid which: hybridizes under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of: SEQ ID NO: 1, 24, 4, 27, or 30; or exhibits identity over a stretch of at least about 30 nucleotides to a primate DCRS3 or DCRS4. Preferred embodiments include those wherein: the wash conditions

are at 45° C and/or 500 mM salt; the wash conditions are at 55° C and/or 150 mM salt; the stretch is at least 55 nucleotides; or the stretch is at least 75 nucleotides.

Other methods include those of modulating physiology or development of a cell or tissue culture cells comprising contacting the cell with an agonist or antagonist of a mammalian DCRS3 or DCRS4. Preferably, the cell is transformed with a nucleic acid encoding a DCRS3 or DCRS4 and another cytokine receptor subunit.

10

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

OUTLINE

- I. General
- 15 II. Activities
- III. Nucleic acids
 - A. encoding fragments, sequence, probes
 - B. mutations, chimeras, fusions
 - C. making nucleic acids
 - 20 D. vectors, cells comprising
- IV. Proteins, Peptides
 - A. fragments, sequence, immunogens, antigens
 - B. muteins
 - C. agonists/antagonists, functional equivalents
 - 25 D. making proteins
- V. Making nucleic acids, proteins
 - A. synthetic
 - B. recombinant
 - C. natural sources
- 30 VI. Antibodies
 - A. polyclonals
 - B. monoclonal
 - C. fragments; Kd
 - D. anti-idiotypic antibodies
 - 35 E. hybridoma cell lines
- VII. Kits and Methods to quantify DCRS
 - A. ELISA
 - B. assay mRNA encoding
 - C. qualitative/quantitative
 - 40 D. kits
- VIII. Therapeutic compositions, methods
 - A. combination compositions
 - B. unit dose
 - C. administration
- 45 IX. Screening

X. Ligands

I. General

The present invention provides the amino acid sequences and
5 DNA sequences of mammalian, herein primate, cytokine receptor-
like subunit molecules, these designated DNAX Cytokine Receptor
Subunit 3 (DCRS3; 50R) and DNAX Cytokine Receptor Subunit 4
(DCRS4; cytor) having particular defined properties, both
structural and biological. Various cDNAs encoding these
10 molecules were obtained from primate, e.g., human, cDNA sequence
libraries. Other primate or other mammalian counterparts would
also be desired.

Some of the standard methods applicable are described or
referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning,
15 A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring
Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A
Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; Ausubel,
et al., Biology, Greene Publishing Associates, Brooklyn, NY; or
Ausubel, et al. (1987 and periodic supplements) Current
20 Protocols in Molecular Biology, Greene/Wiley, New York; each of
which is incorporated herein by reference.

Nucleotide (SEQ ID NO: 1) and corresponding amino acid
sequence (SEQ ID NO: 2) of a human DCRS3 coding segment are
shown in Table 1; likewise for the DCRS3.2 as SEQ ID NO: 24 and
25 25; comparison of DCRS3.1 and DCRS3.2 polypeptide sequences is
shown also in Table 1. Reverse translations based upon the
universal genetic code are provided in Table 2; comparison of
the encoding nucleic acid sequences is also presented in Table
2. The sequences are derived from genomic sequence at
30 chromosome location clones CIT987SK-582J2\ HUAC004525 and CIT987-
SKA-670B5 HUAC002303, at 16p12, and other cDNA sequences. The
predicted signal sequence is indicated, but may depend on cell
type, or may be a few residues in either direction. The
transmembrane segment (SEQ ID NO: 2) is predicted to run from
35 about leu248-ser264 (glu242-his268). Predicted fibronectin
domain runs from about asn128-tyr220; cytokine receptor WS box
from about trp224-ser228; conserved disulfide motif between

cys6-cys26; second conserved disulfide linkage at cys65-cys89; five N glycosylation sites at Asn residues 61, 97, 121, 128, and 145; seven cAMP PK sites at lys4; lys68; lys184; arg191; arg201; lys202; and lys292; fourteen Ca phosphorylation sites at thr71, 5 ser130, ser187, ser205, ser237, ser182, ser195, ser310, ser317, thr323, ser374, ser385, ser403, and thr499; five myristoly sites at gly174, gly303, gly439, gly449, and gly466; four PKC phosphorylation sites at ser7, ser147, ser180, and ser264; and one tyrosine kinase site at lys163.

10 Exon boundaries are predicted to be about between nucleotides g49-c50, g230-g231, g284-g285, a484-g485, g597-a598, g775-a776, g875-g876, and g957-a958. Because the sequences have been derived from genomic sequence, in which the introns have not been spliced out, particularly important compositions will 15 be those which encode segments across the boundaries, e.g., both nucleic acid sequence and amino acid sequence. The segments will comprise, e.g., segments across the boundary which may comprise 8, 9, 11, 13, 15, 17 20, 25, 30, 35, 50, or more nucleotides on either or both sides adjacent to an exon boundary, or 4, 5, 6, 7, or 8 amino acids on either or both 20 sides adjacent a boundary. The lengths on either side need not be the same for purposes of novelty, e.g., three amino acids on one side and 5 on the other side. Thus, e.g., compositions are provided comprising, e.g., 15 contiguous nucleotides across a 25 boundary, of which at least 6 are from each side. Similarly, compositions are provided, e.g., comprising at least 3 amino acids from each side of the exon boundary, with a matching of at least 8 amino acids across the boundary. Also provided are compositions comprising a plurality of such segments across 30 multiple exon boundaries, which different segments need not have the same length limitations. Thus, the invention provides a nucleic acid comprising, e.g., at least 5 nucleotides in each side across the exon 1/2 boundary, and at least 4 nucleotides on either side of the the exon 3/4, 4/5, 5/6, and/or 6/7 35 boundaries. Natural sequence compositions would be preferred.

Nucleotide (SEQ ID NO: 4) and corresponding amino acid sequence (SEQ ID NO: 5) of a human DCRS4 coding segment are

shown in Table 3; likewise for the DCRS4.2 as SEQ ID NO: 27 and 28 and the DCRS4.3 as SEQ ID NO: 30 and 31; comparison of DCRS4 polypeptide sequences is shown also in Table 3. Reverse translations based upon the universal genetic code are provided in Table 4; comparison of the encoding nucleic acid sequences is also presented in Table 4. The sequence of DCRS4.1 is derived from genomic sequence at chromosome location 6q24.1-25.2, within some 50 kb of IFN γ R1 chain. The predicted DCRS4.1 signal sequence is indicated, but may depend on cell type, or may be a few residues in either direction. This embodiment of the receptor lacks a transmembrane segment, which is unusual, but there is precedent for soluble forms of cytokine receptor subunits. See, e.g., IL-12R α (p40 subunit) and the EBI3 receptor subunit homolog. For the DCRS4.1, the predicted cytokine receptor domain from pro10-arg49; conserved disulfide motif between cys57-cys65; five N glycosylation sites at Asn residues 35, 131, 136, 157, and 174; four cAMP PK sites at arg30, lys98, lys106, and lys156; eight Ca phosphorylation sites at thr4, thr60, ser64, thr68, thr71, ser159, ser176, and ser220; three myristoyl sites at gly89, gly103, and gly186; three PKC phosphorylation sites at ser7, ser97, and ser217; one amidation site at tyr79; one cAMP phosphorylation site at lys98; and two CK2 phosphorylation sites at ser3 and ser159. Exon boundaries are predicted to be about between nucleotides c59-a60; t197-a198, g206-a207, g430-c431, and g601-a602. Alignment with the other DCRS4 embodiments is provided. As described above, compositions with sequence across the exon boundaries are provided.

Table 1: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS3.1; 50R). Primate, e.g., human embodiment (see SEQ ID NO: 1 and 2). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

35	atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctc cag gga	48
	Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly	
	-20 -15 -10 -5	
40	gcc ctc gag ggg atg gag agg aag ctc tgc agt ccc aag cca ccc ccc	96
	Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro	
	-1 1 5 10	
	acc aag gcc tct ctc ccc act gac cct cca ggc tgg ggc tgc ccc gac	144

12

	Thr	Lys	Ala	Ser	Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	
			15					20					25				
5	ctc	gtc	tgc	tac	acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	192
	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	
			30					35				40					
10	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	240
	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	
			45			50					55				60		
15	aat	aat	act	ggg	tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	288
	Asn	Asn	Thr	Gly	Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	
					65					70					75		
	gac	cag	tat	gaa	gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	336
	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	
				80					85					90			
20	agg	tgc	gcc	cac	aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	384
	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	
				95				100					105				
25	gta	ttc	cac	ttc	atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	gac	432
	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	
				110				115				120					
30	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	480
	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	
						130					135				140		
35	agc	aga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	528
	Ser	Arg	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	
					145					150					155		
	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac	agg	aac	576
	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	
				160					165					170			
40	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	tca	gtg	624
	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	
				175				180					185				
45	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	ctg	gag	ttc	cgc	aaa	gac	tgc	672
	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys	Asp	Ser	
				190				195				200					
50	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	tcc	tcc	tac	720
	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser	Ser	Tyr	
						210					215					220	
	cag	ggg	acc	tgg	agt	gaa	tgg	agt	gac	ccg	gtc	atc	ttt	cag	acc	cag	768
	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	Thr	Gln	
					225					230					235		
55	tca	gag	gag	tta	aag	gaa	ggc	tgg	aac	cct	cac	ctg	ctg	ctt	ctc	ctc	816
	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu	Leu	Leu	
				240					245					250			
60	ctg	ctt	gtc	ata	gtc	ttc	att	cct	gcc	ttc	tgg	agc	ctg	aag	acc	cat	864

	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys	Thr	His	
			255					260					265				
5	cca	ttg	tgg	agg	cta	tgg	aag	aag	ata	tgg	gcc	gtc	ccc	agc	cct	gag	912
	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser	Pro	Glu	
			270				275					280					
10	cgg	ttc	ttc	atg	ccc	ctg	tac	aag	ggc	tgc	agc	gga	gac	ttc	aag	aaa	960
	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe	Lys	Lys	
						290					295					300	
15	tgg	gtg	ggt	gca	ccc	ttc	act	ggc	tcc	agc	ctg	gag	ctg	gga	ccc	tgg	1008
	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly	Pro	Trp	
					305				310						315		
20	agc	cca	gag	gtg	ccc	tcc	acc	ctg	gag	gtg	tac	agc	tgc	cac	cca	cca	1056
	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His	Pro	Pro	
				320					325					330			
25	cgg	agc	ccg	gcc	aag	agg	ctg	cag	ctc	acg	gag	cta	caa	gaa	cca	gca	1104
	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu	Pro	Ala	
			335				340						345				
30	gag	ctg	gtg	gag	tct	gac	ggt	gtg	ccc	aag	ccc	agc	ttc	tgg	ccg	aca	1152
	Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp	Pro	Thr	
			350				355					360					
35	gcc	cag	aac	tcg	ggg	ggc	tca	gct	tac	agt	gag	gag	agg	gat	cgg	cca	1200
	Ala	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	
					370						375					380	
40	tac	ggc	ctg	gtg	tcc	att	gac	aca	gtg	act	gtg	cta	gat	gca	gag	ggg	1248
	Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Leu	Asp	Ala	Glu	Gly	
					385					390					395		
45	cca	tgc	acc	tgg	ccc	tgc	agc	tgt	gag	gat	gac	ggc	tac	cca	gcc	ctg	1296
	Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Leu	
				400					405					410			
50	gac	ctg	gat	gct	ggc	ctg	gag	ccc	agc	cca	ggc	cta	gag	gac	cca	ctc	1344
	Asp	Leu	Asp	Ala	Gly	Leu	Glu	Pro	Ser	Pro	Gly	Leu	Glu	Asp	Pro	Leu	
				415				420					425				
55	ttg	gat	gca	ggg	acc	aca	gtc	ctg	tcc	tgt	ggc	tgt	gtc	tca	gct	ggc	1392
	Leu	Asp	Ala	Gly	Thr	Thr	Val	Leu	Ser	Cys	Gly	Cys	Val	Ser	Ala	Gly	
			430				435					440					
60	agc	cct	ggg	cta	gga	ggg	ccc	ctg	gga	agc	ctc	ctg	gac	aga	cta	aag	1440
	Ser	Pro	Gly	Leu	Gly	Gly	Pro	Leu	Gly	Ser	Leu	Leu	Asp	Arg	Leu	Lys	
						450					455					460	
65	cca	ccc	ctt	gca	gat	ggg	gag	gac	tgg	gct	ggg	gga	ctg	ccc	tgg	ggt	1488
	Pro	Pro	Leu	Ala	Asp	Gly	Glu	Asp	Trp	Ala	Gly	Gly	Leu	Pro	Trp	Gly	
					465				470						475		

	ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg	1536
	Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu	
	480 485 490	
5	gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac	1584
	Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp	
	495 500 505	
10	tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga	1632
	Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly	
	510 515 520	
15	ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt	1680
	Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu	
	525 530 535 540	
	tcg agc cct gga ccc cag gcc agc taa	1707
	Ser Ser Pro Gly Pro Gln Ala Ser	
	545	
20	MPRGWAAPLLLLLLQGALEGMERKLCSPKPPPTKASLPTDPPGWGCPDLVCYTDYLTQTVICILEMWNLHPSTLTLTW	
	ILSNNTGCYIKDRTLRLQDQYEELKDEATSCSLHRSAHNATHATYTCHMDVHFHMADDIFSVNITDQSGNYSQECG	
	SFLLAESRQYNISWRSDYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLPLLEFRKDSSYELQVR	
	AGPMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLLLLLLVIVFIPAFWSLKTHPLWRLWKKIWA VPSPERFFM	
25	PLYKGCSDGDFKKWVGAPFTGSSLELGPWSPEVPSTLEVYSCHPPRSPAKRLQTELQEPALVESDGVKPSFWPTA	
	QNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDL DAGLEPSGLEDPLLDAGTTVLSCGCVS	
	AGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLMDTDFDSGFVSGDCSSPVECDFTS	
	PGDEGPPRSYLQWVVI PPPLSSPGPQAS	
30	Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like	
	embodiments (DCRS3.2; SEQ ID NO: 24 and 25):	
	atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga	48
	Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly	
35	-20 -15 -10 -5	
	ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96
	Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
	-1 1 5 10	
40	gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144
	Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	
	15 20 25	
45	ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192
	Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	
	30 35 40	
	tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc	240
50	Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	
	45 50 55 60	
	tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc	288
	Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	
55	65 70 75	
	aac atc aca gac cag tct ggc aac tac tcc cag gan tgt ggc agc ttt	336
	Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Xaa Cys Gly Ser Phe	
	80 85 90	
60		

15

	ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384
	Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	
	95 100 105	
5	acc ttc tca gga cag tat aat atn tcc tgg cgc tca gat tac gaa gac	432
	Thr Phe Ser Gly Gln Tyr Asn Xaa Ser Trp Arg Ser Asp Tyr Glu Asp	
	110 115 120	
10	cct gcc ttc tac atg ctg aaa ggc aag ctt caa tat gag ctg cag tac	480
	Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr	
	125 130 135 140	
15	agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc	528
	Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile	
	145 150 155	
20	tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa	576
	Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys	
	160 165 170	
25	gac tcg agc tat gag ctg can gtg cgg gca ggg ccc atg cct ggc tcc	624
	Asp Ser Ser Tyr Glu Leu Xaa Val Arg Ala Gly Pro Met Pro Gly Ser	
	175 180 185	
30	tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc tgt cag	672
	Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Cys Gln	
	190 195 200	
35	acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt	720
	Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu	
	205 210 215 220	
40	ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag	768
	Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys	
	225 230 235	
45	acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc	816
	Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser	
	240 245 250	
50	cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc	864
	Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe	
	255 260 265	
55	aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga	912
	Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly	
	270 275 280	
60	ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac	960
	Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His	
	285 290 295 300	
65	cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa	1008
	Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu	
	305 310 315	

	cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg	1056
	Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp	
	320 325 330	
5	ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat	1104
	Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp	
	335 340 345	
10	cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca	1152
	Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala	
	350 355 360	
15	gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca	1200
	Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro	
	365 370 375 380	
20	gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac	1248
	Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp	
	385 390 395	
25	cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca	1296
	Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser	
	400 405 410	
30	gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga	1344
	Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg	
	415 420 425	
35	cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc	1392
	Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro	
	430 435 440	
40	tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca	1440
	Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser	
	445 450 455 460	
45	ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc	1488
	Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly	
	465 470 475	
50	tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac	1536
	Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp	
	480 485 490	
55	gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg	1584
	Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro	
	495 500 505	
60	cca ctt tcg agc cct gga ccc cag gcc agc taa	1617
	Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser	
	510 515	
65	MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLTQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHA TYTCHMDVHFHMADDIFSVNITDQSGNYSQXCGSFLLAESIKPAPPFNVTVTFSGQYNXSWRSYEDPAFYMLKGKL QYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSYELXVRAGMPGSSYQGTWSEWSDPVICQTQSEELK EGWNPHELLLLLLLVIVFIPAFWSLKTPLWRLWKKIWAVPSPERFFMPLYKGCSDFKKWWGAPFTGSSLELGPWSP EVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGGSAYSEERDRPYGLVSIIDTVTLDAE	

GPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPDLLDAGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPPLADGEDWAGG
LPWGGRRSPGGVSESEAGSPLAGLMDTDFDSGFVSGDCSSPVECDFTSPGDEGPPTSRLRQWVIPPPLSSPGPQAS

Polypeptide sequence comparison of DCRS3.2 and DCRS3.1:

5	DCRS3.2	1	MPRGWAAPLLLLLLQ-----GWGCPDLV	24
	DCRS3.1	1	MPRGWAAPLLLLLLQGALEGMERKLCSPKPPPTKASLPTDPPGWGCPDLV	50

10	DCRS3.2	25	CYTDYLQTVICILEMWNLHPSTLTLTW-----QDQYE	56
	DCRS3.1	51	CYTDYLQTVICILEMWNLHPSTLTLTWILSNNTGCIKDRTLDLRQDQYE	100

15	DCRS3.2	57	ELKDEATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYS	106
	DCRS3.1	101	ELKDEATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYS	150

20	DCRS3.2	107	QXCGSFLLAESIKPAPPFNVTVTFSGQYNXSWRSYEDPAFYMLKGKQY	156
	DCRS3.1	151	QECGSFLLAE-----SRQYNISWRSYEDPAFYMLKGKQY	186
			* *****	
	DCRS3.2	157	ELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSYELXVRAGPMP	206
	DCRS3.1	187	ELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSYELQVRAGPMP	236

25	DCRS3.2	207	GSSYQGTWSEWSDPVICQTQSEELKEGWNPHLLLLLLLLLVIVFIPAFWSLK	256
	DCRS3.1	237	GSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLLLLLLLLVIVFIPAFWSLK	286

30	DCRS3.2	257	THPLWRLWKKIWAVSPERFFMPLYKGCSDGFKKWVGAPFTGSSLELGPW	306
	DCRS3.1	287	THPLWRLWKKIWAVSPERFFMPLYKGCSDGFKKWVGAPFTGSSLELGPW	336

35	DCRS3.2	307	SPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQ	356
	DCRS3.1	337	SPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQ	386

40	DCRS3.2	357	NSGGSAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDA	406
	DCRS3.1	387	NSGGSAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDA	436

	DCRS3.2	407	GLEPSPGLEDPDLLDAGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPPLADG	456
	DCRS3.1	437	GLEPSPGLEDPDLLDAGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPPLADG	486

45	DCRS3.2	457	EDWAGGLPWGGRSPGGVSESEAGSPLAGLMDTDFDSGFVSGDCSSPVECD	506
	DCRS3.1	487	EDWAGGLPWGGRSPGGVSESEAGSPLAGLMDTDFDSGFVSGDCSSPVECD	536

50	DCRS3.2	507	FTSPGDEGPPTSRLRQWVIPPPLSSPGPQAS	538
	DCRS3.1	537	FTSPGDEGPPTSRLRQWVIPPPLSSPGPQAS	568

Table 2: Reverse Translation of primate, e.g., human, DCRS3.1 (SEQ ID NO:
3). N may be A, C, G, or T.

ATGCCNMGGNGTGGGCGNCNCNYTNYTNYTNYTNYTNYTNCARGGNGCNYTNGARGGNATGGARMGNAARYTNTG
YWSNCCNAARCCNCCNCCNACNAARGCNWSNYTNCNACNGAYCCNCCNGGNTGGGGNTGYCCNGAYYTNGTNTGYT
AYACNGAYTAYTNCARACNGTNATHGTGYATHYTNGARATGTGGAAYTNCAYCCNWSNACNYTNACNYTNACNTGG
60 ATHYTNWSNAAYAYACNGGNTGYTAYATHAARGAYMGNACNYTNGAYYTNMGNACARGAYCARTAYGARGARYTNAA

RGAYGARGCNACNWSNTGYWSNYTNCAYMGNWSNGCNCAAYAGCNACNCTAYACNTGYCAYATGGAYG
TNTTYCAYTTYATGGCNGAYGAYATHTTYWSNGTNAAYATHACNGAYCARWSNGGNAAYTAYWSNCARGARTGYGGN
WSNTTTYTNYTNGCNGARWSNMGNCARTAYAAYATHWSNTGGMGNWSNGAYTAYGARGAYCCNGCNTTYTAYATGYT
NAARGGNAARYTNCARTAYGARYTNCARTAYMGNAAYMGNGNGAYCCNTGGGCGNGTWSNCCNMGMGNAAARYTNA
5 THWSNGTNGAYWSNMGNWSNGTWSNYTNYTNCNYTNGARTTYMGNAARGAYWSNWSNTAYGARYTNCARGTMMGN
GCNGGNCNATGCCNGGNWSNWSNTAYCARGGNACNTGGWSNGARTGGWSNGAYCCNGTNAHTTYCARACNCARWS
NGARGARYTNAARGARGGNTGGAAYCCNCAYYTNYTNYTNYTNYTNYTNGTNAHTGNTTYATHCCNGCNTTYT
GGWSNYTNAARACNCAYYCCNYTNTGGMGNYTNTGGAARAARATHTGGGCGNGTNCNWSNCCNGARMGNTTYTTYATG
CCNYTNTAYAARGGNTGYWSNGGNGAYTTYAARAARTGGGTNGGNGCNCNTTYACNGGNWSNWSNYTNGARYTNGG
10 NCCNTGGWSNCCNGARTNCCNWSNACNYTNGARGTNTAYWSNTGYCAYCCNCCNMGNWSNCCNGCNAARMGNYTNC
ARYTNAACNGARYTNCARGARCCNGCNGARYTNGTNGARWSNGAYGGNGTNCNCAARCCNWSNTTYTGGCCNACNGCN
CARAAYSNGGGGNGWSNGCNTAYWSNGARGARMGNGAYMGNCNTAYGGNYTNGTNGWSNATHGAYACNGTNAACNGT
NYTNGAYGCNGARGGNCNTGYACNTGGCCNTGYWSNTGYGARGAYGGNTAYCCNGCNYTNGAYYTNGAYGCNG
GNYTNGARCCNWSNCCNGGNYTNGARGAYCCNYTNGAYGAYGCNGGNACNACNGTNYTNGWSNTGYGGNTGYGTNWSN
15 GCNGGNWSNCCNGGNYTNGGNGGNCNYTNGGNWSNYTNYTNGAYMGNYTNAARCCNCCNYTNGCNGAYGGNGARGA
YTGGGCGNGGNGNYTNCNTGGGGNGGNGMGNWSNCCNGGNGGNTNGWSNGARWSNGARGCGNGNWSNCCNYTNGCNG
GNYTNGAYATGGAYACNTTYGAYWSNGGNTTYGTNGGNWSNGAYTGYWSNWSNCCNGTNGARTGYGAYTTYACNWSN
CCNGGNGAYGARGGNCCNCCNMGNWSNTAYYTNGMNCARTGGGTNGTNAHTCCNCCNCCNYTNGWSNWSNCCNGGNC
NCARGCNWSN

Reverse Translation of primate, e.g., human, DCRS3.2 (SEQ ID NO: 26). N may be A, C, G, or T.

25 ATGCCNMGNGGNTGGGCNGCNCNCTNYTNYTNYTNYTNYTNCARGGNGGNTGGGGNTGYCCNGAYYNTGNTGYTA
YACNGAYTAYYTNCARACNGTNAHTGYATHYNTGARATGTGGAAYYTNCAYCCNWSNACNYTNACNYTNACNTGGC
ARGAYCARTAYGARGARYTNAARGAYGARGCNACNWSNTGYWSNYTNCAYMGNWSNGCNCAYAAAYGCNACNCAYGCN
ACNTAYACNTGYCAYATGGAYGTNTTYCÄYTTYATGGCNGAYGAYATHHTYWSNGTNAAYATHACNGAYCARWSNGG
NAAYTAYWSNCARNNTGYGGNWSNTTYTNYTNGCNGARWSNATHAARCCNGCNCNCNTTYAAYGTNACNGTNA
30 CNTTYWSNGGNCARTAYAAYNWNWSNTGGMGNWSNGAYTAYGARGAYCCNGCNTTYATAYGTYNAAARGGNAARYTN
CARTAYGARYTNCARTAYMGNAAAYMGNGGNGAYCCNTGGCNGTWNWSCNMGNMGNAARYTNATHWSNGTNGAYWS
NMGNWSNGTWSNYTNYTNCNCTNYTNGARTYTMGNAARGAYWSNWSNTAYGARYTNNNGTNGMGNGCNGGNCNATGC
CNGGNWSNWSNTAYCARGGNACNTGGWSNGARTGGWSNGAYCCNGTNAHTGYCARACNCARWSNGARGARYTNAAR
GARGGNTGGAAYCCNCAYYTNYTNYTNYTNYTNYTNYTNGTNGTNAHTGNTTYATHCCNGCNTTYTGGWSNYTNAARAC
35 NCAYCCNYTNTGGMGNYTNTGGAARAARATHTGGGCNGTNCNWSNCCNGARMGNTTYTATYCCCNNTNTAYAARG
GNTGYWSNGGNGAYTTYAARAARTGGGTNGGNGCNCNCTTYACNGGNSWSNWTNGARYTNGGNCNTGGWSNCCN
GARGTNCNWSNACNYTNGARGTNTAYWSNTGYCAYCCNCTNMGNWSNCCNGCNAARMGNYTNCARYTNACNGARYT
NCARGARCCNGCNGARYTNGTNGARWSNGAYGGNGTNCNAAARCCNWSNTTYTGGCCNACNGCNCARAAYWSNGGNG
GNWSNGCNTAYWSNGARGARMGNAYMGNCNTAYGGNYTNGTNGWSNATHGAYACNGTACNGTNYTNGAYGCNGAR
40 GGNCNTGYACNTGGCCNTGYWSNTGYGARGAYGAYGGNTAYCCNGCNYTNGAYYTNGAYGCNGGNYTNGARCCNWS
NCCNGGNYTNGARGAYCCNYTNYTNGAYGCNGGNACNACNGTNYTNGWSNTGYGGNTGYGTNGWSNGCNGGNSNCCNG
GNYTNGGNGGNCNCTYNGGNSWSNYTNYTNGAYMGNYTNAARCCNCTNYTNGCNGAYGGNGARGAYTGGCGNGGNG
YTNCCTYGGGNGGNGMGNWSNCCNGGNGGNTWSNGARWSNGARGCNGGNSNCCNYTNGCNGGNYTNGAYATGGA
YACNTTYGAYWSNGGNTTYGTNGCNWSNGAYTGYWSNWSNCCNGTNGARTGYGAYTTYACNWSNCCNGGNGAYGARG
45 GNCCNCCNMGNWSNTAYYTNGMNCARTGGGTNGTNAHTCCNCCNCTNYTNGWSNWSNCCNGGNCNCARGCNWSN

Nucleic acid sequence comparison of two DCRS3 embodiments:

50	DCRS3.2	1	ATGCCGCGTGGCTGGGCCGCCCCCTTGCTCCTGCTGCTGCTCCAGGGAGC	50
	DCRS3.1	1	ATGCCGCGTGGCTGGGCCGCCCCCTTGCTCCTGCTGCTGCTCCAGGGA--	49

	DCRS3.2	51	CCTCGAGGGGATGGAGAGGAAGCTCTGCAGTCCCAAGCCACCCCCACCA	100
	DCRS3.1	49	-----	49

55

	DCRS3.2	101	AGGCCTCTCTCCCCACTGACCCTCCAGGCTGGGGCTGCCCCGACCTCGTC	150
	DCRS3.1	50	-----GCTGGGGCTGCCCCGACCTCGTC	72

5	DCRS3.2	151	TGCTACACCGATTACCTCCAGACGGTCATCTGCATCCTGGAAATGTGGAA	200
	DCRS3.1	73	TGCTACACCGATTACCTCCAGACGGTCATCTGCATCCTGGAAATGTGGAA	122

10	DCRS3.2	201	CCTCCACCCCAGCACGCTCACCTTACCTGGATACTTTCTAATAATACTG	250
	DCRS3.1	123	CCTCCACCCCAGCACGCTCACCTTACCTGG-----	153

	DCRS3.2	251	GGTGCTATATCAAGGACAGAACACTGGACCTCAGGCAAGACCAGTATGAA	300
15	DCRS3.1	154	-----CAAGACCAGTATGAA	168

	DCRS3.2	301	GAGCTGAAGGACGAGGCCACCTCCTGCAGCCTCCACAGGTCGGCCCCACAA	350
20	DCRS3.1	169	GAGCTGAAGGACGAGGCCACCTCCTGCAGCCTCCACAGGTCGGCCCCACAA	218

	DCRS3.2	351	TGCCACGCATGCCACCTACACCTGCCACATGGATGTATTCCACTTCATGG	400
	DCRS3.1	219	TGCCACGCATGCCACCTACACCTGCCACATGGATGTATTCCACTTCATGG	268

25	DCRS3.2	401	CCGACGACATTTTCAGTGTCAACATCACAGACCAGTCTGGCAACTACTCC	450
	DCRS3.1	269	CCGACGACATTTTCAGTGTCAACATCACAGACCAGTCTGGCAACTACTCC	318

30	DCRS3.2	451	CAGGAGTGTGGCAGCTTTCTCCTGGCTGAGAGCA-----	484
	DCRS3.1	319	CAGGANTGTGGCAGCTTTCTCCTGGCTGAGAGCATCAAGCCGGCTCCCC	368

	DCRS3.2	485	-----GACAGTATAATATCTCCTGGCGCT	508
35	DCRS3.1	369	TTTCAACGTGACTGTGACCTTCTCAGGACAGTATAATATNTCCTGGCGCT	418

	DCRS3.2	509	CAGATTACGAAGACCCTGCCTTCTACATGCTGAAGGGCAAGCTTCAGTAT	558
40	DCRS3.1	419	CAGATTACGAAGACCCTGCCTTCTACATGCTGAAGGGCAAGCTTCAATAT	468

	DCRS3.2	559	GAGCTGCAGTACAGGAACCGGGGAGACCCCTGGGCTGTGAGTCCGAGGAG	608
	DCRS3.1	469	GAGCTGCAGTACAGGAACCGGGGAGACCCCTGGGCTGTGAGTCCGAGGAG	518

45	DCRS3.2	609	AAAGCTGATCTCAGTGGACTCAAGAAGTGTCTCCCTCCTCCCCCTGGAGT	658
	DCRS3.1	519	AAAGCTGATCTCAGTGGACTCAAGAAGTGTCTCCCTCCTCCCCCTGGAGT	568

50	DCRS3.2	659	TCCGCAAAGACTCGAGCTATGAGCTGCAGGTGCGGGCAGGGCCCATGCCT	708
	DCRS3.1	569	TCCGCAAAGACTCGAGCTATGAGCTGCANGTGCGGGCAGGGCCCATGCCT	618

	DCRS3.2	709	GGCTCCTCCTACCAGGGGACCTGGAGTGAATGGAGTGACCCGGTCATCTT	758
55	DCRS3.1	619	GGCTCCTCCTACCAGGGGACCTGGAGTGAATGGAGTGACCCGGTCATCTG	668

	DCRS3.2	759	TCAGACCCAGTCAGAGGAGTTAAAGGAAGGCTGGAACCCCTCACCTGCTGC	808
	DCRS3.1	669	TCAGACCCAGTCAGAGGAGTTAAAGGAAGGCTGGAACCCCTCACCTGCTGC	718

5	DCRS3.2	809	TTCTCCTCCTGCTTGTTCATAGTCTTCATTCTGCTTCTGGAGCCTGAAG	858
	DCRS3.1	719	TTCTCCTCCTGCTTGTTCATAGTCTTCATTCTGCTTCTGGAGCCTGAAG	768

10	DCRS3.2	859	ACCCATCCATTGTGGAGGCTATGGAAGAAGATATGGGCCGTCCCCAGCCC	908
	DCRS3.1	769	ACCCATCCATTGTGGAGGCTATGGAAGAAGATATGGGCCGTCCCCAGCCC	818

15	DCRS3.2	909	TGAGCGGTTCTTCATGCCCTGTACAAGGGCTGCAGCGGAGACTTCAAGA	958
	DCRS3.1	819	TGAGCGGTTCTTCATGCCCTGTACAAGGGCTGCAGCGGAGACTTCAAGA	868

20	DCRS3.2	959	AATGGGTGGGTGCACCCTTCACTGGCTCCAGCCTGGAGCTGGGACCCTGG	1008
	DCRS3.1	869	AATGGGTGGGTGCACCCTTCACTGGCTCCAGCCTGGAGCTGGGACCCTGG	918

25	DCRS3.2	1009	AGCCCAGAGGTGCCCTCCACCCTGGAGGTGTACAGCTGCCACCCACCACG	1058
	DCRS3.1	919	AGCCCAGAGGTGCCCTCCACCCTGGAGGTGTACAGCTGCCACCCACCACG	968

30	DCRS3.2	1059	GAGCCCGGCCAAGAGGCTGCAGCTCACGGAGCTACAAGAACCAGCAGAGC	1108
	DCRS3.1	969	GAGCCCGGCCAAGAGGCTGCAGCTCACGGAGCTACAAGAACCAGCAGAGC	1018

35	DCRS3.2	1109	TGGTGGAGTCTGACGGTGTGCCCAAGCCCAGCTTCTGGCCGACAGCCCAG	1158
	DCRS3.1	1019	TGGTGGAGTCTGACGGTGTGCCCAAGCCCAGCTTCTGGCCGACAGCCCAG	1068

40	DCRS3.2	1159	AACTCGGGGGGCTCAGCTTACAGTGAGGAGAGGGATCGGCCATACGGCCT	1208
	DCRS3.1	1069	AACTCGGGGGGCTCAGCTTACAGTGAGGAGAGGGATCGGCCATACGGCCT	1118

45	DCRS3.2	1209	GGTGTCCATTGACACAGTGACTGTGCTAGATGCAGAGGGGCCATGCACCT	1258
	DCRS3.1	1119	GGTGTCCATTGACACAGTGACTGTGCTAGATGCAGAGGGGCCATGCACCT	1168

50	DCRS3.2	1259	GGCCCTGCAGCTGTGAGGATGACGGCTACCCAGCCCTGGACCTGGATGCT	1308
	DCRS3.1	1169	GGCCCTGCAGCTGTGAGGATGACGGCTACCCAGCCCTGGACCTGGATGCT	1218

55	DCRS3.2	1309	GGCCTGGAGCCCAGCCCAGGCCCTAGAGGACCCACTCTTGATGCAGGGAC	1358
	DCRS3.1	1219	GGCCTGGAGCCCAGCCCAGGCCCTAGAGGACCCACTCTTGATGCAGGGAC	1268

55	DCRS3.2	1359	CACAGTCCTGTCCTGTGGCTGTGTCTCAGCTGGCAGCCCTGGGCTAGGAG	1408
	DCRS3.1	1269	CACAGTCCTGTCCTGTGGCTGTGTCTCAGCTGGCAGCCCTGGGCTAGGAG	1318

55	DCRS3.2	1409	GGCCCCTGGGAAGCCTCCTGGACAGACTAAAGCCACCCCTTGACATGGG	1458
	DCRS3.1	1319	GGCCCCTGGGAAGCCTCCTGGACAGACTAAAGCCACCCCTTGACATGGG	1368

DCRS3.2 1459 GAGGACTGGGCTGGGGGACTGCCCTGGGGTGGCCGGTCACCTGGAGGGGT 1508
 DCRS3.1 1369 GAGGACTGGGCTGGGGGACTGCCCTGGGGTGGCCGGTCACCTGGAGGGGT 1418

5 DCRS3.2 1509 CTCAGAGAGTGAGGCGGGCTACCCCTGGCCGGCCTGGATATGGACACGT 1558
 DCRS3.1 1419 CTCAGAGAGTGAGGCGGGCTACCCCTGGCCGGCCTGGATATGGACACGT 1468

10 DCRS3.2 1559 TTGACAGTGGCTTTGTGGGCTCTGACTGCAGCAGCCCTGTGGAGTGTGAC 1608
 DCRS3.1 1469 TTGACAGTGGCTTTGTGGGCTCTGACTGCAGCAGCCCTGTGGAGTGTGAC 1518

15 DCRS3.2 1609 TTCACCAGCCCCGGGGACGAAGGACCCCCCGGAGCTACCTCCGCCAGTG 1658
 DCRS3.1 1519 TTCACCAGCCCCGGGGACGAAGGACCCCCCGGAGCTACCTCCGCCAGTG 1568

20 DCRS3.2 1659 GGTGGTCATTCTCCGCCACTTTCGAGCCCTGGACCCCAGGCCAGCTAA 1707
 DCRS3.1 1569 GGTGGTCATTCTCCGCCACTTTCGAGCCCTGGACCCCAGGCCAGCTAA 1617

Table 3: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiment 4 (DCRS4.1; cytor). Primate, e.g., human embodiment (see SEQ ID NO: 4 and 5). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt 48
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 -20 -15 -10

30 act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 -5 -1 1 5 10

35 agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 15 20 25

40 cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 30 35 40

45 aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 45 50 55

50 act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 60 65 70 75

55 gaa cct tat tac ggg agg agg ggc aaa aat aaa aat aaa ggg aat cct 336
 Glu Pro Tyr Tyr Gly Arg Arg Gly Lys Asn Lys Asn Lys Gly Asn Pro
 80 85 90

55 tgg ggg cca aaa caa agt aaa cgg aaa tca aag ggg aac cag aag acc 384
 Trp Gly Pro Lys Gln Ser Lys Arg Lys Ser Lys Gly Asn Gln Lys Thr
 95 100 105

	aac aca gtg act gcc cca gct gcc ctg aag gca ttt gct gga tgt gca	432
	Asn Thr Val Thr Ala Pro Ala Ala Leu Lys Ala Phe Ala Gly Cys Ala	
	110 115 120	
5	aaa ata gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg	480
	Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu	
	125 130 135	
10	ttg gta att ctc cat gct cca aat tta cca tat aga tac caa aag gaa	528
	Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu	
	140 145 150 155	
15	aaa aat gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt	576
	Lys Asn Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe	
	160 165 170	
20	ata att aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct	624
	Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala	
	175 180 185	
25	cac aga gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt	672
	His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys	
	190 195 200	
30	gta gtg gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga	720
	Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg	
	205 210 215	
35	agt gaa gag aga tgt gtg gaa att cca tga	750
	Ser Glu Glu Arg Cys Val Glu Ile Pro	
	220 225	
40	MMPKHCFLGLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNLQWQPGRALTGNSSVYFVQYKIYGQRQWKNKED CWGTQELSCDLTSETSDIQEPYYGRRGKKNKGNPNWGPQSKRKSNGNQKTNTVTAPAALKAFAGCAKIDPPVMNIT QVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQ PMLDRRSQRSEERCVEIP.	
45	Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS4.2, cytorX700; SEQ ID NO: 27 and 28):	
50	ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGAACCTCAGTCAACGCA TGAGTCTCTGAAGCCTCAGAGGGTACAATTTTCAGTCCCGAAAATTTTCAACATTTTGCAATGGCAGCCCGGGAGGG CACTTACTGGCAACAGCAGTGTCTATTTGTGCAGTACAAAATATATGGACAGAGACAATGGAAAAATAAAGAAGAC TGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGT GAGGGCGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAG ATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCAAATTTACCATATAGA TACCAAAAGGAAAAAATGTATCTATAGAAGATTACTATGAATACTATAACCGAGTTTATATAATTAACAATTCCT AGAAAAGGAGCAAAAGGTTTATGAAGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCCA TGA	
55	atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt	48
	Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
	-20 -15 -10	
60	act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
	Thr Gly Val Ala Gly Thr Gln Ser Thr His Ser Leu Lys Pro Gln	
	-5 -1 1 5 10	

23

	agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
	Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
	15 20 25	
5	ccc ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
	Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
	30 35 40	
10	aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
	Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
	45 50 55	
15	act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
	Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
	60 65 70 75	
20	gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
	Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
	80 85 90	
25	gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
	Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
	95 100 105	
30	gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
	Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
	110 115 120	
35	att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
	Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
	125 130 135	
40	gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
	Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
	140 145 150 155	
45	aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
	Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
	160 165 170	
50	gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
	Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
	175 180 185	
55	gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa	672
	Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	
	190 195 200	
60	gag aga tgt gtg gaa att cca tga	696
	Glu Arg Cys Val Glu Ile Pro	
	205 210	
65	>cytorX700	
70	MMPKHCFGLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNLQWQPGRALTGNSSVYFVQYKIYQQRQWKNKED	
75	CWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPPWETKIDPPVMNITQVNGSLLVILHAPNLPYR	
80	YQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRRAVEIEALTPHSSYCVVAEIIYQPMLDRRSQRSEERCVEIP	

Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS4.3 cytorX600; SEQ ID NO: 30 and 31):

5 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTTTTTCTTACTGGTGTAGCAGGAACCTCAGTCAACGCA
 TGAGTCTCTGAAGCCTCAGAGGGTACAATTTTCAGTCCCGAAATTTTCAACATTTTGCAATGGCAGCCTGGGAGGG
 CACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATATATGGACAGAGACAATGGAAAAATAAGAAGAC
 TGTGTTGGGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAACCTCAGACATACAGGAATCTTATTACGGGAGGGT
 GAGGGCGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCCTCCCTGGTGGGAAAGAGCAAAAG
 10 GTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAAT
 ATATCAGCCACGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCCATGA

 atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttt ttc ctt 48
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 -20 -15 -10
 15 act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 -5 -1 1 5 10
 20 agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 15 20 25
 25 cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 30 35 40
 30 aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 45 50 55
 act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 60 65 70 75
 35 gaa tct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca 336
 Glu Ser Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 80 85 90
 40 gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aga gca aaa 384
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys
 95 100 105
 45 ggt tta tgaaggggct cacagagcgg ttgaaattga agctctaaca ccacactcca 440
 Gly Leu
 gctactgtgt agtggctgaa atatatcagc ccacgtaga cagaagaagt cagagaagt 500
 aagagagatg tgtggaaatt ccatga 526
 50
 >cytorX600
 MMPKHCFGLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNLQWQPGRALTGNSVYFVQYKIYQQRQWKNKED
 CWGTQELSCDLTSETSDIQESYYGRVRAASAGSYSEWSMTPRFTPWWERAKGL.
 55 Polypeptide sequence comparison of DCRS4.1, DCRS4.2 and DCRS4.3:

5 DCRS4.1 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILOWQPG 50
DCRS4.2 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILOWQPG 50
DCRS4.3 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILOWQPG 50

10 DCRS4.1 51 RALTGNSSVYFVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYY 100
DCRS4.2 51 RALTGNSSVYFVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYY 100
DCRS4.3 51 RALTGNSSVYFVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQESYY 100

15 DCRS4.1 101 GR-RGKNKNKGNPWGPKQSKRKSNGNKTNTVTAPAALKAFAGCAKIDPP 149
DCRS4.2 101 GRVRAASAGSYSEWS--MTPRFTP-----WWETKIDPP 131
DCRS4.3 101 GRVRAASAGSYSEWS--MTPRFTP-----WWE----- 119
** * . * .

20 DCRS4.1 150 VMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLE 199
DCRS4.2 132 VMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLE 181
DCRS4.3 123 -----RAKGL 130
.. *..

25 DCRS4.1 200 KEQKVYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSEERCVEIP 249
DCRS4.2 182 KEQKVYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSEERCVEIP 231
DCRS4.3 131 130

Table 4: Reverse Translation of primate, e.g., human, DCRS4.1 (SEQ ID NO: 6).
N may be A, C, G, or T.

30 ATGATGCCNAARCAITGYTTYTNGGNTTYTNTATHWSNTTYTTYTNACNGGNGTNGCNGGNACNCARWSNACNCA
YGARWSNYTNAARCCNCARMGNGTNCARTTYCARWSNMGNAAITTYCAYAAAYATHYTNCARTGGCARCCNGGNGMNG
CNYTNACNGGNAAYWSNWSNGTNTAYTTYGTNCARTAYAAARATHAYGGNCARMGNCARTGGAARAAAYARGARGAY
TGYTGGGGNACNCARGARYTNWSNTGYGAYTNACNWSNGARACNWSNGAYATHCARGARCCNTAYTAYGGNMGMNG
35 NGGNAARAAAYAAARAAAYARGGNAAYCCNTGGGGNCCNAARCARWSNAAARMGNARWSNAAARGGNAAYCARAARACNA
AYACNGTNACNGCNCNGCNGCNYTNAARGCNTTYGCGNGGNTGYCNAARATHGAYCCNCCNGTNGTATGAAYATHACN
CARGTNAAYGGNWSNYTNTYTNATHTYTNCAAYGCNCCNAAYTNCNTAYMGNTAYCARAARGARAARAYGTNWS
NATHGARGAYTAYTAYGARYTNTYTNATMGNGTNTTYATHATHAAAYWSNYTNGARAARGARCARAARGTNTAYG
40 ARGGNGCNCAYMGNGCNGTNGARATHGARGCNYTNACNCCNCAYSNWSNTAYTGYGTNGTNGCNGARATHAYCAR
CCNATGYTNGAYMGNGNWSNCAARMGNWSNGARGARMGNTGYGTNGARATHCCN

Reverse Translation of primate, e.g., human, DCRS4.2 (SEQ ID NO: 29).
N may be A, C, G, or T.

45 ATGATGCCNAARCAITGYTTYTNGGNTTYTNTATHWSNTTYTTYTNACNGGNGTNGCNGGNACNCARWSNACNCA
YGARWSNYTNAARCCNCARMGNGTNCARTTYCARWSNMGNAAITTYCAYAAAYATHYTNCARTGGCARCCNGGNGMNG
CNYTNACNGGNAAYWSNWSNGTNTAYTTYGTNCARTAYAAARATHAYGGNCARMGNCARTGGAARAAAYARGARGAY
TGYTGGGGNACNCARGARYTNWSNTGYGAYTNACNWSNGARACNWSNGAYATHCARGARCCNTAYTAYGGNMGMNGT
50 NMGNGCNGCNGNWSNGCNGGNGNWSNTAYWSNGARTGGWSNATGACNCCNMGNTTYACNCCNTGGTGGGARACNAARATHG
AYCCNCCNGTNGTATGAAYATHACNARGTNAAYGGNWSNYTNTYTNATHTYTNCAAYGCNCCNAAYTNCNTAYMGNT
TAYCARAARGARAARAYGTNWSNATHGARGAYTAYTAYGARYTNTYTNATMGNGTNTTYATHATHAAAYWSNYT
NGARAARGARCARAARGTNTAYGARGGNGCNCAYMGNGCNGTNGARATHGARGCNYTNACNCCNCAYSNWSNTAYT
GYGTNGTNGCNGARATHAYCARCCNATGYTNGAYMGNGNWSNCAARMGNWSNGARGARMGNTGYGTNGARATHCCN

55 Reverse Translation of primate, e.g., human, DCRS4.3 (SEQ ID NO: 32). N may
be A, C, G, or T.

60 ATGATGCCNAARCAITGYTTYTNGGNTTYTNTATHWSNTTYTTYTNACNGGNGTNGCNGGNACNCARWSNACNCA
YGARWSNYTNAARCCNCARMGNGTNCARTTYCARWSNMGNAAITTYCAYAAAYATHYTNCARTGGCARCCNGGNGMNG
CNYTNACNGGNAAYWSNWSNGTNTAYTTYGTNCARTAYAAARATHAYGGNCARMGNCARTGGAARAAAYARGARGAY

TGYTGGGGNACNCARGARYTNWSNTGYGAYYTNACNWSNGARACNWSNGAYATHCARGARWSNTAYTAYGGNMGNGT
 NMGNCGCNCNWSNGCNGGNWSNTAYWSNGARTGGWSNATGACNCCNMGNNTTYACNCCNTGGTGGGARMGNGCNAARG
 GNYTN

5 Nucleic acid sequence comparison of three DCRS4 embodiments:

10	DCRS4.1	1	ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTAC	50
	DCRS4.2	1	ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTAC	50
	DCRS4.3	1	ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTTTCTTCCTTAC	50

15	DCRS4.1	51	TGGTGTAGCAGGAACCTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGG	100
	DCRS4.2	51	TGGTGTAGCAGGAACCTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGG	100
	DCRS4.3	51	TGGTGTAGCAGGAACCTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGG	100

20	DCRS4.1	101	TACAATTTCAGTCCCGAAATTTTCAACAATTTTGCAATGGCAGCCTGGG	150
	DCRS4.2	101	TACAATTTCAGTCCCGAAATTTTCAACAATTTTGCAATGGCAGCCTGGG	150
	DCRS4.3	101	TACAATTTCAGTCCCGAAATTTTCAACAATTTTGCAATGGCAGCCTGGG	150

25	DCRS4.1	151	AGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATATA	200
	DCRS4.2	151	AGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATATA	200
	DCRS4.3	151	AGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATATA	200

30	DCRS4.1	201	TGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAAC	250
	DCRS4.2	201	TGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAAC	250
	DCRS4.3	201	TGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAAC	250

35	DCRS4.1	251	TCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTAC	300
	DCRS4.2	251	TCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTAC	300
	DCRS4.3	251	TCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAATCTTATTAC	300

40	DCRS4.1	301	GGGAGGAGGGGCAAAAATAAAAATAAAGGGAATCCTTGGGGGCCAAAACA	350
	DCRS4.2	301	GGGAGGGTG-----AGGGCGGCCTCGGC-----	323
	DCRS4.3	301	GGGAGGGTG-----AGGGCGGCCTCGGC-----	323
***** *				
45	DCRS4.1	351	AAGTAAACGGAAATCAAAGGGGAACCAGAAGACCAACACAGTGACTGCC	400
	DCRS4.2	324	---TGGGAGCTACTCAGAAATGGAGCATGA-----CGCCGCGGTTCACT	363
	DCRS4.3	324	---TGGGAGCTACTCAGAAATGGAGCATGA-----CGCCGCGGTTCACT	363
* * * * *				
50	DCRS4.1	401	CAGCTGCCCTGAAGGCATTTGCTGGATGTGCAAAAATAGATCCTCCAGTC	450
	DCRS4.2	364	C-----CCTGGTGGGAA-----ACAAAATAGATCCTCCAGTC	396
	DCRS4.3	364	C-----CCTGGTGGGAAAGAGCAAAAGGTTTATGAAGGGGCTCACAGA-	406
* **** * *				
55	DCRS4.1	451	ATGAATATAACCCAAGTC--AATGGCTCTTTGTTGGTAATTCTCCATGCT	498
	DCRS4.2	397	ATGAATATAACCCAAGTC--AATGGCTCTTTGTTGGTAATTCTCCATGCT	444
	DCRS4.3	407	GCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGC	456
* * * * *				

DCRS4.1	499	CCAAATTTACCATATAGATACCAAAAGGAAAAAATGTATCTATAGAAGA	548
DCRS4.2	445	CCAAATTTACCATATAGATACCAAAAGGAAAAAATGTATCTATAGAAGA	494
DCRS4.3	457	TGAAATATATCA-GCCCACGTTAGACAGAAGAAGTCAGAGAAGT-GAAGA	504
5		**** * * * * * * * * * * * * * * * *	
DCRS4.1	549	TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCAGTAGAAA	598
DCRS4.2	495	TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCAGTAGAAA	544
DCRS4.3	505	GAGATGTGTGGAAATTCATGA	526
10		* * * * *	
DCRS4.1	599	AGGAGCAAAAGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCT	648
DCRS4.2	545	AGGAGCAAAAGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCT	594
DCRS4.3	527		526
15			
DCRS4.1	649	CTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAATATATCAGCCCAT	698
DCRS4.2	595	CTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAATATATCAGCCCAT	644
DCRS4.3	527		526
20			
DCRS4.1	699	GTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCAT	748
DCRS4.2	645	GTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCAT	694
DCRS4.3	527		526
25			
DCRS4.1	749	GA 750	
DCRS4.2	695	GA 696	
DCRS4.3	527	526	
30			

Table 5: Alignment of various cytokine receptor subunits with DCRS3.1.
 IL-2R is SEQ ID NO: 7; IL-9R is SEQ ID NO: 8; GM/IL-3/5 receptor b
 subunit common (ILRbc) is SEQ ID NO: 9; TPOR is SEQ ID NO: 10; and IL-7R
 is SEQ ID NO: 11 (see GenBank).

IL-2R_HU	VNG--TSQFTC---FYNSTRANISCVWSQ-DGALQDTSCQVHAWPDRRRWN-----QTC
DCRS3_HU	LCS--PKPPPT----KASLPTDPPGWC-PDLVCYTDYLQTVICILEMWN---LHP--STL
IL-9R_HU	ICI----C-TC-----VCLGVSVTGEQGPRSRFTCLTNILRIDCHWS---APELGQG
40 ILRbc_HU	ILTPNGNEDTTADFFLTMTPTDSLVSST-LPLPEVQCFVFNVEYMNCTWNSSEPQPTNL
TPOR_HU	LLASDSEPLKC---FSRTFEDLTCFWDE-EEAAPSGTYQLLYAYPREKPR--ACP--LSS
IL-7R_HU	VSGESGYAQNG---DLEDAELDDYSFSC-YSQLEVNGSQHSLTCAFEDPD-----VN
45 IL-2R_HU	ELLPVSQASWACN-----LILG-----APDS--QKLTTVD-----IV
DCRS3_HU	TLTWILSNNTGCIYKDR----TDLRQ-DQYE--ELKDEA-TSCSLHR-----SAHNAT
IL-9R_HU	SSPWLLFTSNQAPG----G-THKCILR--GSECTVVLPE--AVLVPSD-----NFT
ILRbc_HU	TLHYWYKNSDNDK-----VQKCSHY-----LFSEEITSGCQLQK-K---EIHLYQ
TPOR_HU	QSMPHFGTRYVCQFPDQ--EEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSII
50 IL-7R_HU	TTNLEFEICGALV-----EVKCLNFR-----KLQEIYFIETKKFL-----LI
IL-2R_HU	TLRVLCREGVRWRV---MAIQDFKPFENLRLMAPISLQV---VHVETHRCNIS---WEI
DCRS3_HU	HATYTCHMDVVFHF---MADDIFS--VNITDQSGNYSQECGSFLLAESRQYNIS---WRS
55 IL-9R_HU	ITFHHCMMSGREQVS---LVDPEYLPRRHVKLDPPSDLQS-----NISSGHCILT---WSI
ILRbc_HU	TFVVQLQDPREPRR---QATQMLKLQNLVIPWAPENLTL---HKLSQSLELN---WNN
TPOR_HU	KAMGGSQPGELQISWEEPAPEISDFLRYELRYGPRDPKNS---TGPTVIQLIATETCCPA
IL-7R_HU	GKSNICVK-VGEKS---LTCKKIDLTITIVKPEAPFDLSVI---YREGANDFVVT---FNT

```

IL-2R_HU  SQASHYFERHLE---FEARTLSPGHTWEEAPLLTLK-----QKQEWICLETILT-PDTQ
DCRS3_HU  DYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLIS-----VDSRSVSLPLLEFRKDSS
IL-9R_HU  SPALEPMTTLLS---YELAFKKQEEAWEQAQHRDHIV-----G-VTWLILEAFELDPGFI
5  ILRbc_HU  RFLNHCLEHLV-----QYRTD---WDHSWTEQSV-----DYRHKFSLPSVDGQKRYT
TPOR_HU   LQRPHSASALD-----QSPCAQPTMPWQDGPQKQTSREASALTAEGGSCLISGLQPGNS
IL-7R_HU  SHLQKKYVKVLMHD-VAYRQEKDENKWTNVLSST-----KLTLQLRK--LQPAAM
          *

10  IL-2R_HU  YEFQVRVKPLQGEFT-----TWSPWSQPLAFRTKPAALG
DCRS3_HU  YELQVRAGPMPGSSYQG-----TWSEWSDPVIFQTQSEELK
IL-9R_HU  HEARLRVQMATLEDDVVEEERYTGQWSEWSQPVCQAPQRQGP
ILRbc_HU  FRVRSRFNPLCGSAQ-----HWSEWSHPHWSNNTSKEN
TPOR_HU   YWLQLRSEPDGSLGG-----SWGWSLPVTVDLPGDAVA
15  IL-7R_HU  YEIKVRSIPDHYFKG-----FWSEWSPSYFRTPEINNS
          . : *          * . ** .

```

Alignment of various cytokine receptor subunits with DCRS4.1. IL-10Rb is the beta subunit of IL-10R, human is SEQ ID NO: 12, mouse is SEQ ID NO: 13; INaR1 is the beta subunit of IFNa with human SEQ ID NO: 14 and mouse SEQ ID NO: 15; INgR is interferon gamma receptor subunit alpha with human SEQ ID NO: 16 and mouse SEQ ID NO: 17; IL-10Ra is the alpha receptor subunit with mouse SEQ ID NO: 18 and human SEQ ID NO: 19; INgS (SEQ ID NO: 20) is the beta receptor subunit for INFg; Zcytor7 (SEQ ID NO: 21) and CYTOR11 (SEQ ID NO: 22) are from patent filings from Zymogenetics, and INaR2 (SEQ ID NO: 23) is the beta subunit of the receptor for IFNa.

```

IL-10Rb_Hu  PENVRMNSVNFKNILQWES-PAFAKGNL--TFTAQYLSY-----RIFQDKCMNTTL
30  IL-10Rb_Mu  PEKVRMNSVNFKNILQWEV-PAFPKTNL--TFTAQYESY-----RSFQDHCKRTAS
INaR1_HU     POKVEVDIIDNFI LRWNR-SDES VGNV--TFSFDYQKTGMD----NWIKLSGCQNITS
INaR1_MU     PENIDVYIIDNNTLKWSS-HGESMGSV--TFSAEYRTKDEA----KWLKVPECQHTTT
INgR_HU      PTNVTIESYNMNPIVWEY-QIMPQVP---VFTVEVKNYGVK----NSEWIDACINISH
INgR_MU      PTNVLIKSYNLNPVVCWEY-QNMSQTP---IFTVQVKVY-----SGSWTDSCTNISD
35  IL-10Ra_Mu  PSYVWFEARFFQHILHWKP-IPNQSEST--YYEVALKQYGNS----TWNDIHCIRKAQA
IL-10Ra_Hu   PPSVWFEEAEFFHHILHWTP-IPNQSEST--CYEVALLRYGIE----SWNSISNC--SQT
INgS_HU      PLNPRHLHYNDEQILTWEP-SPSSNDPRPVVYQVEYSFIDGSW---HRLLEPNCTDITE
Zcytor7_Hu   PANITFLSINMKNVLQWTPPEGLQGVK--TYTVQYFIYGQK----KWLNKSECRNINR
CYTOR11_HU   LQHVKFQSSNFENILTWDS-GPEGTPDT--VYSIEYKTYGER----DWVAKKGCQRITR
40  INaR2_HU    SCTFKISLRNFRSILSWEL-KNHSIVPTHYTLTYTMSKPE-----DLKVVKNCANTTR
DCRS4.1_HU   PQRVQFQSRNFHNLQWQPGRALTGNSS--VYFVQYKIYGQR----QWKNKEDCWGTQE
          . : *          *

```

```

IL-10Rb_Hu  TECDFSSLSK-----YGDHTLRVRAEFADEHSDWVNIT-FCPVDDTIIGPPG--MQVEV
45  IL-10Rb_Mu  TQCDFSHLSK-----YGDYTVRVRAELADEHSEWVNVT-FCPVEDTIIGPPE--MQIES
INaR1_HU     TKCNFSSSLKLN----VYEEIKLRIRAEKEN-TSSWYEVDSFTPFRAQIGPPE--VHLEA
INaR1_MU     TKCEFSLLDTN----VYIKTQFRVRAEENGSTSSWNEVDPIPFYTAHMSPE--VRLEA
INgR_HU      HVCNISDHVGDP----SNSLWVRVKARVGQKESAYAKSEEFVAVCRDGKIGPPKLDIR-KE
INgR_MU      HCCNIYGQIMYP----DVSAWARVKAVGQKESDYARSKEFLMCLKGKVGPPGLEIRRK
50  IL-10Ra_Mu  LSCDLTTFTLDLYHR-SYGYRARVRAVDNSQYSNWTTTTETRTVDEVILTVD--VTLKA
IL-10Ra_Hu   LSYDLTAVTLDLYH--SNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLTVGS--VNLEI
INgS_HU      TKCDLTGGGRLKLFHPFTVFLRVRAKGNLTSKWVGLEPFQHYENVTVGPPKN--ISVTP
Zcytor7_Hu   TYCDLSAETSDY----EHQYAKVKAIWGTCKSKWAESGRFYPFLETQIGPPE--VALTT
CYTOR11_HU   KSCNLTVETGN----LTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDV--TCISK
55  INaR2_HU    SFCDLTDEWRS-----THEAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPE--FEIVG
DCRS4.1_HU   LSCDLTSETSD-----IQEPYYGRRGKNKKNPNWGPQSKRKSNGNQTNTVT--APAAL
          : :

```

	IL-10Rb_Hu	LADSLHMRFLAPKIENEYE---TWTMKNVYNSWTYNVQYWKNGTDEKFQ-ITPQYDFEVL
	IL-10Rb_Mu	LAESLHLRFSAPQIENEPE---TWTLKNIYDSWAYRVQYWKNGTNEKFQ-VVSPYDSEVL
	INaR1_HU	EDKAIVIHISPGTKDSV-----MWALD--GLSFTYSLLIWKNSSGVEER-IENIYSRHKI
5	INaR1_MU	EDKAILVHISPPGQDGN-----MWALE--KPSFSYTIRIWQKSSSDKKT-INSTYYVEKI
	IngR_HU	EKQIMIDIFHPSVVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGS-EIQY-KILTQKEDDC
	IngR_MU	EEQLSVLVFHPVNVNGESQGTMTFGDGSTCYTFDYTVYVEHNRSGEILH-TKHTVEKEEC
	IL-10Ra_Mu	MDGIIYGTIHPPRPTITPA--GDEYEQVFKDLRVYKISIRKFS--ELKN-ATKRVKQETF
	IL-10Ra_Hu	HNGFILGKIQLPRPKMAPA--NDTYESIFSHFREYEIAIRKVPK-NFTF-THKKVKHENF
10	IngS_HU	GKGS�VIHFSPPFDFVHG-----ATFQYLVHYWEKSETQEQE-VEGPFKSNIS
	Zcytor7_Hu	DEKSISVVLTAPEKWKRNPELPSVMQIYSNLKYNVSVLNTKSNRTWS-QCVTNHTLV
	CYTOR11_HU	VRSIQMIHVHTPTPIRAGDG-HRLTLEDIFHDLFPYHLELQVNRITYQMHL-GGKQREYEFF
	INaR2_HU	FTNHINVMVKFPSIVEEEL-----Q---FDLSLVIEEQSEGIVKKHKPEIKGNMSGNF
15	DCRS4.1_HU	KAFAGCAKIDPPVMNITQ-----VNGSLLVILHAPNLPYRYQ-KEKNVSIEDY
		:
	IL-10Rb_Hu	RN-----LEPWTTYCVQVRGFLPDRN-----KAGEWSEPVC EQ
	IL-10Rb_Mu	RN-----LEPWTTYCIQVQGFLLDQN-----RTGEWSEPICER
	INaR1_HU	YK-----LSPETTYCLKVKAALLTSW-----KIGVYSPVHCIK
20	INaR1_MU	PE-----LLPETTYCLEVKAIHPSLK-----KHSNYSTVQCIS
	IngR_HU	DEIQCQLAI-----PVSSLNSQYCVSAEGVLHVWG-----VTTEKSKEVCIT
	IngR_MU	NETLCELNI-----SVSTLDSRYCISVDGISSFQW-----VRTEKSKDVCIP
	IL-10Ra_Mu	TLT-----VPIGVKRFCKVKLPRLSRI-----NKAEWSEEQCLL
	IL-10Ra_Hu	SLL-----TSGEVGEFCVQVKPSVASRS-----NKGWWSKEECIS
25	IngS_HU	VLG-----NLKPYRVYCLQTEAQLILKNKK-----IRPHGLLSNVSCHE
	Zcytor7_Hu	TW-----LEPNTLYCVHVESFVPGPP-----RRAQPSEKQCAR
	CYTOR11_HU	GLTPDTEFLGTIMICVPTWAKESAPYMC RVKTL PDRTWTYSFSGAFLFSMGFLVAVLCYL
	INaR2_HU	TYIID-----KLIPNTNYCVSVYLEHSDEQ-----AVIKSPLKCTL
30	DCRS4.1_HU	YE-----LLYRVFIINNSLE-----KEQKVYEGAHRA
	IL-10Rb_Hu	TTHDETVP-
	IL-10Rb_Mu	TGNDEITP-
	INaR1_HU	TTVENELPP
35	INaR1_MU	TTVANKMPV
	IngR_HU	IFNSSIKG-
	IngR_MU	PFHDDRKD-
	IL-10Ra_Mu	ITTEQYFT-
	IL-10Ra_Hu	LT-RQYFT-
40	IngS_HU	TTANASAR-
	Zcytor7_Hu	TLKDQSSE-
	CYTOR11_HU	SYRYVTKPP
	INaR2_HU	LPPGQES
45	DCRS4.1_HU	VEIEALTP-

Table 5 shows comparison of sequences of cytokine receptor subunits with the primate, e.g., human, DCRS3.1 (50R), and DCRS4.1 (cytor). Both of the new genes are likely alpha type
50 receptor subunits, and thus should bind to ligand without the need for a beta subunit. Based upon structural features, the ligand for the DCRS3 subunits are likely to be a member of the family of cytokines which includes IL-2, IL-4, IL-7, IL-9, and the additional cytokines which signal through IL-2γ common

receptor-like subunits IL-13, IL-15, and the TSLP ligand. Similarly, the ligand for the DCRS4 receptor subunits are probably a ligand in the IL-10 or IFN families, which may be a multi-subunit cytokine, analogous to IL-6 and IL-12.

5 As used herein, the term DCRS3 shall be used to describe a protein comprising an amino acid sequence shown in Table 1; likewise with DCRS4 and Table 3. In many cases, a substantial fragment thereof will be functionally or structurally
10 equivalent, including, e.g., an extracellular or intracellular domain. The invention also includes a protein variation of a DCRS3 allele whose sequence is provided, e.g., a mutein or soluble extracellular construct. Typically, such agonists or antagonists will exhibit less than about 10% sequence
15 substitutions, e.g., 2-, 3-, 5-, 7-fold, and others. It also encompasses allelic and other variants, e.g., natural polymorphic, of the protein described. Typically, it will bind to its corresponding biological ligand, perhaps in a dimerized state with an alpha receptor subunit, with high affinity, e.g.,
20 at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. The term shall also be used herein to refer to related naturally occurring forms, e.g., alleles, polymorphic variants, and metabolic variants of the mammalian
25 protein. Preferred forms of the receptor complexes will bind the appropriate ligand with an affinity and selectivity appropriate for a ligand-receptor interaction.

This invention also encompasses combinations of proteins or peptides having substantial amino acid sequence identity with
30 the amino acid sequences in Tables 1 or 3. It will include sequence variants with relatively few substitutions, e.g., preferably less than about 3-5.

A substantial polypeptide "fragment", or "segment", is a stretch of amino acid residues of at least about 8 amino acids,
35 generally at least 10 amino acids, more generally at least 12 amino acids, often at least 14 amino acids, more often at least 16 amino acids, typically at least 18 amino acids, more

typically at least 20 amino acids, usually at least 22 amino acids, more usually at least 24 amino acids, preferably at least 26 amino acids, more preferably at least 28 amino acids, and, in particularly preferred embodiments, at least about 30 or more amino acids. Sequences of segments of different proteins can be compared to one another over appropriate length stretches. In many situations, fragments may exhibit functional properties of the intact subunits, e.g., the extracellular domain of the transmembrane receptor may retain the ligand binding features, and may be used to prepare a soluble receptor-like complex.

Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches. In some comparisons, gaps may be introduced, as required. See, e.g., Needleham, et al., (1970) J. Mol. Biol. 48:443-453; Sankoff, et al., (1983) chapter one in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group (GCG), Madison, WI; each of which is incorporated herein by reference. This changes when considering conservative substitutions as matches. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Homologous amino acid sequences are intended to include natural allelic and interspecies variations in the cytokine sequence. Typical homologous proteins or peptides will have from 50-100% homology (if gaps can be introduced), to 60-100% homology (if conservative substitutions are included) with an amino acid sequence segment of Table 1 or 3. Homology measures will be at least about 70%, generally at least 76%, more generally at least 81%, often at least 85%, more often at least 88%, typically at least 90%, more typically at least 92%, usually at least 94%, more usually at least 95%, preferably at least 96%, and more preferably at least 97%, and in particularly preferred embodiments, at least 98% or more. The degree of homology will

vary with the length of the compared segments. Homologous proteins or peptides, such as the allelic variants, will share most biological activities with the embodiments described in Table 1 or 3.

5 As used herein, the term "biological activity" is used to describe, without limitation, effects on inflammatory responses, innate immunity, and/or morphogenic development by cytokine-like ligands. For example, these receptors should mediate phosphatase or phosphorylase activities, which activities are
10 easily measured by standard procedures. See, e.g., Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature
15 363:736-738. The receptors, or portions thereof, may be useful as phosphate labeling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognizing antibodies, or antigens capable of binding
20 antibodies.

The terms ligand, agonist, antagonist, and analog of, e.g., a DCRS3, include molecules that modulate the characteristic cellular responses to cytokine ligand proteins, as well as molecules possessing the more standard structural binding
25 competition features of ligand-receptor interactions, e.g., where the receptor is a natural receptor or an antibody. The cellular responses likely are typically mediated through receptor tyrosine kinase pathways.

Also, a ligand is a molecule which serves either as a
30 natural ligand to which said receptor, or an analog thereof, binds, or a molecule which is a functional analog of the natural ligand. The functional analog may be a ligand with structural modifications, or may be a wholly unrelated molecule which has a molecular shape which interacts with the appropriate ligand
35 binding determinants. The ligands may serve as agonists or antagonists, see, e.g., Goodman, et al. (eds. 1990) Goodman &

Gilman's: The Pharmacological Bases of Therapeutics, Pergamon Press, New York.

Rational drug design may also be based upon structural studies of the molecular shapes of a receptor or antibody and other effectors or ligands. See, e.g., Herz, et al. (1997) J. Recept. Signal Transduct. Res. 17:671-776; and Chaiken, et al. (1996) Trends Biotechnol. 14:369-375. Effectors may be other proteins which mediate other functions in response to ligand binding, or other proteins which normally interact with the receptor. One means for determining which sites interact with specific other proteins is a physical structure determination, e.g., x-ray crystallography or 2 dimensional NMR techniques. These will provide guidance as to which amino acid residues form molecular contact regions. For a detailed description of protein structural determination, see, e.g., Blundell and Johnson (1976) Protein Crystallography, Academic Press, New York, which is hereby incorporated herein by reference.

II. Activities

The cytokine receptor-like proteins will have a number of different biological activities, e.g., modulating cell proliferation, or in phosphate metabolism, being added to or removed from specific substrates, typically proteins. Such will generally result in modulation of an inflammatory function, other innate immunity response, or a morphological effect, as typical of cytokine or interleukin signaling. The subunit may have a specific low affinity binding to the ligand.

The receptors may signal through the JAK pathway. See, e.g., Ihle, et al. (1997) Stem Cells 15(suppl. 1):105-111; Silvennoinen, et al. (1997) APMIS 105:497-509; Levy (1997) Cytokine Growth Factor Review 8:81-90; Winston and Hunter (1996) Current Biol. 6:668-671; Barrett (1996) Baillieres Clin. Gastroenterol. 10:1-15; and Briscoe, et al. (1996) Philos. Trans. R. Soc. Lond. B. Biol. Sci. 351:167-171.

The biological activities of the cytokine receptor subunits will be related to addition or removal of phosphate moieties to substrates, typically in a specific manner, but occasionally in

a non specific manner. Substrates may be identified, or conditions for enzymatic activity may be assayed by standard methods, e.g., as described in Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San

- 5 Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738.

10 The receptor subunits may combine with other subunits, e.g., beta subunits, to form functional complexes, e.g., which may be useful for binding ligand or preparing antibodies. These will have substantial diagnostic uses, including detection or quantitation.

15 III. Nucleic Acids

This invention contemplates use of isolated nucleic acid or fragments, e.g., which encode these or closely related proteins, or fragments thereof, e.g., to encode a corresponding polypeptide, preferably one which is biologically active. In
20 addition, this invention covers isolated or recombinant DNAs which encode combinations of such proteins or polypeptides having characteristic sequences, e.g., of DCRS3s or DCRS4s. Typically, the nucleic acid is capable of hybridizing, under appropriate conditions, with a nucleic acid sequence segment
25 shown in Tables 1 or 3, but preferably not with a corresponding segment of other receptors, e.g., described in Table 5. Said biologically active protein or polypeptide can be a full length protein, or fragment, and will typically have a segment of amino acid sequence highly homologous, e.g., exhibiting significant
30 stretches of identity, to ones shown in Tables 1 or 3. Further, this invention covers the use of isolated or recombinant nucleic acid, or fragments thereof, which encode proteins having fragments which are equivalent to DCRS3 or DCRS4 proteins. The isolated nucleic acids can have the respective regulatory
35 sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others from the natural gene. Combinations, as described, are also provided.

An "isolated" nucleic acid is a nucleic acid, e.g., an RNA, DNA, or a mixed polymer, which is substantially pure, e.g., separated from other components which naturally accompany a native sequence, such as ribosomes, polymerases, and flanking genomic sequences from the originating species. The term
5 embraces a nucleic acid sequence which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates, which are thereby distinguishable from naturally occurring compositions, and chemically synthesized
10 analogs or analogs biologically synthesized by heterologous systems. A substantially pure molecule includes isolated forms of the molecule, either completely or substantially pure.

An isolated nucleic acid will generally be a homogeneous composition of molecules, but will, in some embodiments, contain
15 heterogeneity, preferably minor. This heterogeneity is typically found at the polymer ends or portions not critical to a desired biological function or activity.

A "recombinant" nucleic acid is typically defined either by its method of production or its structure. In reference to its
20 method of production, e.g., a product made by a process, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence. Typically this intervention involves in vitro manipulation, although under certain circumstances it may involve more
25 classical animal breeding techniques. Alternatively, it can be a nucleic acid made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude products of nature, e.g., naturally occurring mutants as found in their natural state.
30 Thus, for example, products made by transforming cells with an unnaturally occurring vector is encompassed, as are nucleic acids comprising sequence derived using any synthetic oligonucleotide process. Such a process is often done to replace a codon with a redundant codon encoding the same or a
35 conservative amino acid, while typically introducing or removing a restriction enzyme sequence recognition site. Alternatively, the process is performed to join together nucleic acid segments

of desired functions to generate a single genetic entity comprising a desired combination of functions not found in the commonly available natural forms, e.g., encoding a fusion protein. Restriction enzyme recognition sites are often the target of such artificial manipulations, but other site specific targets, e.g., promoters, DNA replication sites, regulation sequences, control sequences, or other useful features may be incorporated by design. A similar concept is intended for a recombinant, e.g., fusion, polypeptide. This will include a dimeric repeat. Specifically included are synthetic nucleic acids which, by genetic code redundancy, encode equivalent polypeptides to fragments of DCRS3 or DCRS4 and fusions of sequences from various different related molecules, e.g., other cytokine receptor family members.

A "fragment" in a nucleic acid context is a contiguous segment of at least about 17 nucleotides, generally at least 21 nucleotides, more generally at least 25 nucleotides, ordinarily at least 30 nucleotides, more ordinarily at least 35 nucleotides, often at least 39 nucleotides, more often at least 45 nucleotides, typically at least 50 nucleotides, more typically at least 55 nucleotides, usually at least 60 nucleotides, more usually at least 66 nucleotides, preferably at least 72 nucleotides, more preferably at least 79 nucleotides, and in particularly preferred embodiments will be at least 85 or more nucleotides. Typically, fragments of different genetic sequences can be compared to one another over appropriate length stretches, particularly defined segments such as the domains described below.

A nucleic acid which codes for a DCRS3 or DCRS4 will be particularly useful to identify genes, mRNA, and cDNA species which code for itself or closely related proteins, as well as DNAs which code for polymorphic, allelic, or other genetic variants, e.g., from different individuals or related species. Preferred probes for such screens are those regions of the interleukin which are conserved between different polymorphic variants or which contain nucleotides which lack specificity, and will preferably be full length or nearly so. In other

situations, polymorphic variant specific sequences will be more useful.

This invention further covers recombinant nucleic acid molecules and fragments having a nucleic acid sequence identical to or highly homologous to the isolated DNA set forth herein. In particular, the sequences will often be operably linked to DNA segments which control transcription, translation, and DNA replication. These additional segments typically assist in expression of the desired nucleic acid segment.

Homologous, or highly identical, nucleic acid sequences, when compared to one another, e.g., DCRS3 sequences, exhibit significant similarity. The standards for homology in nucleic acids are either measures for homology generally used in the art by sequence comparison or based upon hybridization conditions. Comparative hybridization conditions are described in greater detail below.

Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 60% of the nucleotides, generally at least 66%, ordinarily at least 71%, often at least 76%, more often at least 80%, usually at least 84%, more usually at least 88%, typically at least 91%, more typically at least about 93%, preferably at least about 95%, more preferably at least about 96 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides, including, e.g., segments encoding structural domains such as the segments described below. Alternatively, substantial identity will exist when the segments will hybridize under selective hybridization conditions, to a strand or its complement, typically using a sequence derived from Tables 1 or 3. Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, more typically at least about 65%, preferably at least about 75%, and more preferably at least about 90%. See, Kanehisa (1984) Nucl. Acids Res. 12:203-213, which is incorporated herein by

reference. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be over a stretch of at least about 17 nucleotides, generally at least about 20 nucleotides, ordinarily at least about 24
5 nucleotides, usually at least about 28 nucleotides, typically at least about 32 nucleotides, more typically at least about 40 nucleotides, preferably at least about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides. This includes, e.g., 125, 150, 175, 200, 225, 250, 275, 300, 325,
10 350, 375, 400, 425, 450, 475, 500, 525, 544, and other lengths.

Stringent conditions, in referring to homology in the hybridization context, will be stringent combined conditions of salt, temperature, organic solvents, and other parameters typically controlled in hybridization reactions. Stringent
15 temperature conditions will usually include temperatures in excess of about 30 °C, more usually in excess of about 37 °C, typically in excess of about 45 °C, more typically in excess of about 55 °C, preferably in excess of about 65 °C, and more preferably in excess of about 70 °C. Stringent salt conditions
20 will ordinarily be less than about 500 mM, usually less than about 400 mM, more usually less than about 300 mM, typically less than about 200 mM, preferably less than about 100 mM, and more preferably less than about 80 mM, even down to less than about 20 mM. However, the combination of parameters is much
25 more important than the measure of any single parameter. See, e.g., Wetmur and Davidson (1968) J. Mol. Biol. 31:349-370, which is hereby incorporated herein by reference.

The isolated DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide insertions, and
30 inversions of nucleotide stretches. These modifications result in novel DNA sequences which encode this protein or its derivatives. These modified sequences can be used to produce mutant proteins (muteins) or to enhance the expression of variant species. Enhanced expression may involve gene
35 amplification, increased transcription, increased translation, and other mechanisms. Such mutant DCRS-like derivatives include predetermined or site-specific mutations of the protein or its

fragments, including silent mutations using genetic code degeneracy. "Mutant DCRS3" as used herein encompasses a polypeptide otherwise falling within the homology definition of the DCRS3 as set forth above, but having an amino acid sequence which differs from that of other cytokine receptor-like proteins as found in nature, whether by way of deletion, substitution, or insertion. In particular, "site specific mutant DCRS3" encompasses a protein having substantial sequence identity with a protein of Table 1, and typically shares most of the biological activities or effects of the forms disclosed herein. Likewise in reference to DCRS4.

Although site specific mutation sites are predetermined, mutants need not be site specific. Mammalian DCRS3 mutagenesis can be achieved by making amino acid insertions or deletions in the gene, coupled with expression. Substitutions, deletions, insertions, or many combinations may be generated to arrive at a final construct. Insertions include amino- or carboxy- terminal fusions. Random mutagenesis can be conducted at a target codon and the expressed mammalian DCRS3 mutants can then be screened for the desired activity, providing some aspect of a structure-activity relationship. Methods for making substitution mutations at predetermined sites in DNA having a known sequence are well known in the art, e.g., by M13 primer mutagenesis. See also Sambrook, et al. (1989) and Ausubel, et al. (1987 and periodic Supplements).

The mutations in the DNA normally should not place coding sequences out of reading frames and preferably will not create complementary regions that could hybridize to produce secondary mRNA structure such as loops or hairpins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Polymerase chain reaction (PCR) techniques can often be applied in mutagenesis. Alternatively, mutagenesis primers are commonly used methods for generating defined mutations at predetermined sites. See, e.g., Innis, et al. (eds. 1990) PCR
5 Protocols: A Guide to Methods and Applications Academic Press, San Diego, CA; and Dieffenbach and Dveksler (1995; eds.) PCR
Primer: A Laboratory Manual Cold Spring Harbor Press, CSH, NY.

Certain embodiments of the invention are directed to combination compositions comprising the receptor or ligand
10 sequences described. In other embodiments, functional portions of the sequences may be joined to encode fusion proteins. In other forms, variants of the described sequences may be substituted.

15 IV. Proteins, Peptides

As described above, the present invention encompasses primate DCRS3, e.g., whose sequences are disclosed in Table 1, and described above. Allelic and other variants are also contemplated, including, e.g., fusion proteins combining
20 portions of such sequences with others, including, e.g., epitope tags and functional domains.

The present invention also provides recombinant proteins, e.g., heterologous fusion proteins using segments from these primate or rodent proteins. A heterologous fusion protein is a
25 fusion of proteins or segments which are naturally not normally fused in the same manner. Thus, the fusion product of a DCRS3 with another cytokine receptor is a continuous protein molecule having sequences fused in a typical peptide linkage, typically made as a single translation product and exhibiting properties,
30 e.g., sequence or antigenicity, derived from each source peptide. A similar concept applies to heterologous nucleic acid sequences. Combinations of various designated proteins into complexes are also provided.

In addition, new constructs may be made from combining
35 similar functional or structural domains from other related proteins, e.g., cytokine receptors or Toll-like receptors, including species variants. For example, ligand-binding or

other segments may be "swapped" between different new fusion polypeptides or fragments. See, e.g., Cunningham, et al. (1989) Science 243:1330-1336; and O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992, each of which is incorporated herein by
5 reference. Thus, new chimeric polypeptides exhibiting new combinations of specificities will result from the functional linkage of receptor-binding specificities. For example, the ligand binding domains from other related receptor molecules may be added or substituted for other domains of this or related
10 proteins. The resulting protein will often have hybrid function and properties. For example, a fusion protein may include a targeting domain which may serve to provide sequestering of the fusion protein to a particular subcellular organelle.

Candidate fusion partners and sequences can be selected
15 from various sequence data bases, e.g., GenBank, c/o IntelliGenetics, Mountain View, CA; and BCG, University of Wisconsin Biotechnology Computing Group, Madison, WI, which are each incorporated herein by reference. In particular, combinations of polypeptide sequences provided in Tables 1 and 3
20 are particularly preferred. Variant forms of the proteins may be substituted in the described combinations.

The present invention particularly provides muteins which bind cytokine-like ligands, and/or which are affected in signal transduction. Structural alignment of human DCRS3 or DCRS4 with
25 other members of the cytokine receptor family show conserved features/residues. See Table 5. Alignment of human DCRS3 or DCRS4 sequence with other members of the cytokine receptor family indicates various structural and functionally shared features. See also, Bazan, et al. (1996) Nature 379:591; Lodi,
30 et al. (1994) Science 263:1762-1766; Sayle and Milner-White (1995) TIBS 20:374-376; and Gronenberg, et al. (1991) Protein Engineering 4:263-269.

Substitutions with either mouse sequences or human sequences are particularly preferred. Conversely, conservative
35 substitutions away from the ligand binding interaction regions will probably preserve most signaling activities; and

conservative substitutions away from the intracellular domains will probably preserve most ligand binding properties.

"Derivatives" of primate DCRS3 include amino acid sequence mutants, glycosylation variants, metabolic derivatives and
5 covalent or aggregative conjugates with other chemical moieties. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in DCRS3 amino acid side chains or at the N- or C- termini, e.g., by means which are well known in the art. These derivatives can include, without
10 limitation, aliphatic esters or amides of the carboxyl terminus, or of residues containing carboxyl side chains, O-acyl derivatives of hydroxyl group-containing residues, and N-acyl derivatives of the amino terminal amino acid or amino-group containing residues, e.g., lysine or arginine. Acyl groups are
15 selected from the group of alkyl-moieties, including C3 to C18 normal alkyl, thereby forming alkanoyl aroyl species.

In particular, glycosylation alterations are included, e.g., made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing, or in further
20 processing steps. Particularly preferred means for accomplishing this are by exposing the polypeptide to glycosylating enzymes derived from cells which normally provide such processing, e.g., mammalian glycosylation enzymes. Deglycosylation enzymes are also contemplated. Also embraced are
25 versions of the same primary amino acid sequence which have other minor modifications, including phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

A major group of derivatives are covalent conjugates of the
30 receptors or fragments thereof with other proteins of polypeptides. These derivatives can be synthesized in recombinant culture such as N- or C-terminal fusions or by the use of agents known in the art for their usefulness in cross-linking proteins through reactive side groups. Preferred
35 derivatization sites with cross-linking agents are at free amino groups, carbohydrate moieties, and cysteine residues.

Fusion polypeptides between the receptors and other homologous or heterologous proteins are also provided. Homologous polypeptides may be fusions between different receptors, resulting in, for instance, a hybrid protein exhibiting binding specificity for multiple different cytokine ligands, or a receptor which may have broadened or weakened specificity of substrate effect. Likewise, heterologous fusions may be constructed which would exhibit a combination of properties or activities of the derivative proteins. Typical examples are fusions of a reporter polypeptide, e.g., luciferase, with a segment or domain of a receptor, e.g., a ligand-binding segment, so that the presence or location of a desired ligand may be easily determined. See, e.g., Dull, et al., U.S. Patent No. 4,859,609, which is hereby incorporated herein by reference. Other gene fusion partners include glutathione-S-transferase (GST), bacterial β -galactosidase, trpE, Protein A, β -lactamase, alpha amylase, alcohol dehydrogenase, and yeast alpha mating factor. See, e.g., Godowski, et al. (1988) Science 241:812-816. Labeled proteins will often be substituted in the described combinations of proteins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Such polypeptides may also have amino acid residues which have been chemically modified by phosphorylation, sulfonation, biotinylation, or the addition or removal of other moieties, particularly those which have molecular shapes similar to phosphate groups. In some embodiments, the modifications will be useful labeling reagents, or serve as purification targets, e.g., affinity ligands.

Fusion proteins will typically be made by either recombinant nucleic acid methods or by synthetic polypeptide

methods. Techniques for nucleic acid manipulation and expression are described generally, for example, in Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), Vols. 1-3, Cold Spring Harbor Laboratory, and Ausubel, et al. (eds. 1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York, which are each incorporated herein by reference. Techniques for synthesis of polypeptides are described, for example, in Merrifield (1963) J. Amer. Chem. Soc. 85:2149-2156; Merrifield (1986) Science 232: 341-347; and Atherton, et al. (1989) Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford; each of which is incorporated herein by reference. See also Dawson, et al. (1994) Science 266:776-779 for methods to make larger polypeptides.

This invention also contemplates the use of derivatives of a DCRS3 or DCRS4 other than variations in amino acid sequence or glycosylation. Such derivatives may involve covalent or aggregative association with chemical moieties. These derivatives generally fall into three classes: (1) salts, (2) side chain and terminal residue covalent modifications, and (3) adsorption complexes, for example with cell membranes. Such covalent or aggregative derivatives are useful as immunogens, as reagents in immunoassays, or in purification methods such as for affinity purification of a receptor or other binding molecule, e.g., an antibody. For example, a cytokine ligand can be immobilized by covalent bonding to a solid support such as cyanogen bromide-activated Sepharose, by methods which are well known in the art, or adsorbed onto polyolefin surfaces, with or without glutaraldehyde cross-linking, for use in the assay or purification of a cytokine receptor, antibodies, or other similar molecules. The ligand can also be labeled with a detectable group, for example radioiodinated by the chloramine T procedure, covalently bound to rare earth chelates, or conjugated to another fluorescent moiety for use in diagnostic assays.

A combination, e.g., including a DCRS3 or DCRS4, of this invention can be used as an immunogen for the production of

antisera or antibodies specific, e.g., capable of distinguishing between other cytokine receptor family members, for the combinations described. The complexes can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies, e.g., Fab, Fab2, Fv, etc. A purified DCRS3 can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. Additionally, DCRS3 fragments may also serve as immunogens to produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies having binding affinity to or being raised against the amino acid sequences shown in Table 1, fragments thereof, or various homologous peptides. In particular, this invention contemplates antibodies having binding affinity to, or having been raised against, specific fragments which are predicted to be, or actually are, exposed at the exterior protein surface of a native DCRS3. Complexes of combinations of proteins will also be useful, and antibody preparations thereto can be made.

The blocking of physiological response to the receptor ligands may result from the inhibition of binding of the ligand to the receptor, likely through competitive inhibition. Thus, in vitro assays of the present invention will often use antibodies or antigen binding segments of these antibodies, or fragments attached to solid phase substrates. These assays will also allow for the diagnostic determination of the effects of either ligand binding region mutations and modifications, or other mutations and modifications, e.g., which affect signaling or enzymatic function.

This invention also contemplates the use of competitive drug screening assays, e.g., where neutralizing antibodies to the receptor complexes or fragments compete with a test compound for binding to a ligand or other antibody. In this manner, the

neutralizing antibodies or fragments can be used to detect the presence of a polypeptide which shares one or more binding sites to a receptor and can also be used to occupy binding sites on a receptor that might otherwise bind a ligand.

5

V. Making Nucleic Acids and Protein

DNA which encodes the protein or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or by screening genomic libraries prepared from a wide variety of cell
10 lines or tissue samples. Natural sequences can be isolated using standard methods and the sequences provided herein, e.g., in Tables 1 or 3. Other species counterparts can be identified by hybridization techniques, or by various PCR techniques, combined with or by searching in sequence databases, e.g.,
15 GenBank.

This DNA can be expressed in a wide variety of host cells for the synthesis of a full-length receptor or fragments which can in turn, for example, be used to generate polyclonal or monoclonal antibodies; for binding studies; for construction and
20 expression of modified ligand binding or kinase/phosphatase domains; and for structure/function studies. Variants or fragments can be expressed in host cells that are transformed or transfected with appropriate expression vectors. These molecules can be substantially free of protein or cellular
25 contaminants, other than those derived from the recombinant host, and therefore are particularly useful in pharmaceutical compositions when combined with a pharmaceutically acceptable carrier and/or diluent. The protein, or portions thereof, may be expressed as fusions with other proteins. Combinations of
30 the described proteins, or nucleic acids encoding them, are particularly interesting.

Expression vectors are typically self-replicating DNA or RNA constructs containing the desired receptor gene or its fragments, usually operably linked to suitable genetic control
35 elements that are recognized in a suitable host cell. These control elements are capable of effecting expression within a suitable host. The multiple genes may be coordinately

expressed, and may be on a polycistronic message. The specific type of control elements necessary to effect expression will depend upon the eventual host cell used. Generally, the genetic control elements can include a prokaryotic promoter system or a eukaryotic promoter expression control system, and typically include a transcriptional promoter, an optional operator to control the onset of transcription, transcription enhancers to elevate the level of mRNA expression, a sequence that encodes a suitable ribosome binding site, and sequences that terminate transcription and translation. Expression vectors also usually contain an origin of replication that allows the vector to replicate independently of the host cell.

The vectors of this invention include those which contain DNA which encodes a combination of proteins, as described, or a biologically active equivalent polypeptide. The DNA can be under the control of a viral promoter and can encode a selection marker. This invention further contemplates use of such expression vectors which are capable of expressing eukaryotic cDNAs coding for such proteins in a prokaryotic or eukaryotic host, where the vector is compatible with the host and where the eukaryotic cDNAs are inserted into the vector such that growth of the host containing the vector expresses the cDNAs in question. Usually, expression vectors are designed for stable replication in their host cells or for amplification to greatly increase the total number of copies of the desirable gene per cell. It is not always necessary to require that an expression vector replicate in a host cell, e.g., it is possible to effect transient expression of the protein or its fragments in various hosts using vectors that do not contain a replication origin that is recognized by the host cell. It is also possible to use vectors that cause integration of the protein encoding portions into the host DNA by recombination.

Vectors, as used herein, comprise plasmids, viruses, bacteriophage, integratable DNA fragments, and other vehicles which enable the integration of DNA fragments into the genome of the host. Expression vectors are specialized vectors which contain genetic control elements that effect expression of

operably linked genes. Plasmids are the most commonly used form of vector but all other forms of vectors which serve an equivalent function and which are, or become, known in the art are suitable for use herein. See, e.g., Pouwels, et al. (1985 and Supplements) Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., and Rodriguez, et al. (eds. 1988) Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Butterworth, Boston, which are incorporated herein by reference.

Transformed cells are cells, preferably mammalian, that have been transformed or transfected with vectors constructed using recombinant DNA techniques. Transformed host cells usually express the desired proteins, but for purposes of cloning, amplifying, and manipulating its DNA, do not need to express the subject proteins. This invention further contemplates culturing transformed cells in a nutrient medium, thus permitting the proteins to accumulate. The proteins can be recovered, either from the culture or, in certain instances, from the culture medium.

For purposes of this invention, nucleic sequences are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to a polypeptide if it is expressed as a preprotein or participates in directing the polypeptide to the cell membrane or in secretion of the polypeptide. A promoter is operably linked to a coding sequence if it controls the transcription of the polypeptide; a ribosome binding site is operably linked to a coding sequence if it is positioned to permit translation. Usually, operably linked means contiguous and in reading frame, however, certain genetic elements such as repressor genes are not contiguously linked but still bind to operator sequences that in turn control expression.

Suitable host cells include prokaryotes, lower eukaryotes, and higher eukaryotes. Prokaryotes include both gram negative and gram positive organisms, e.g., E. coli and B. subtilis. Lower eukaryotes include yeasts, e.g., S. cerevisiae and Pichia, and species of the genus Dictyostelium. Higher eukaryotes include established tissue culture cell lines from animal cells,

both of non-mammalian origin, e.g., insect cells, and birds, and of mammalian origin, e.g., human, primates, and rodents.

Prokaryotic host-vector systems include a wide variety of vectors for many different species. As used herein, E. coli and
5 its vectors will be used generically to include equivalent vectors used in other prokaryotes. A representative vector for amplifying DNA is pBR322 or many of its derivatives. Vectors that can be used to express the receptor or its fragments include, but are not limited to, such vectors as those
10 containing the lac promoter (pUC-series); trp promoter (pBR322-trp); Ipp promoter (the pIN-series); lambda-pP or pR promoters (pOTS); or hybrid promoters such as ptac (pDR540). See Brosius, et al. (1988) "Expression Vectors Employing Lambda-, trp-, lac-, and Ipp-derived Promoters", in Vectors: A
15 Survey of Molecular Cloning Vectors and Their Uses, (eds. Rodriguez and Denhardt), Butterworth, Boston, Chapter 10, pp. 205-236, which is incorporated herein by reference.

Lower eukaryotes, e.g., yeasts and Dictyostelium, may be transformed with DCRS3 or DCRS4 sequence containing vectors.
20 For purposes of this invention, the most common lower eukaryotic host is the baker's yeast, Saccharomyces cerevisiae. It will be used to generically represent lower eukaryotes although a number of other strains and species are also available. Yeast vectors typically consist of a replication origin (unless of the
25 integrating type), a selection gene, a promoter, DNA encoding the receptor or its fragments, and sequences for translation termination, polyadenylation, and transcription termination. Suitable expression vectors for yeast include such constitutive promoters as 3-phosphoglycerate kinase and various other
30 glycolytic enzyme gene promoters or such inducible promoters as the alcohol dehydrogenase 2 promoter or metallothionine promoter. Suitable vectors include derivatives of the following types: self-replicating low copy number (such as the YRp-series), self-replicating high copy number (such as the
35 YEep-series); integrating types (such as the YIp-series), or mini-chromosomes (such as the YCp-series).

Higher eukaryotic tissue culture cells are normally the preferred host cells for expression of the functionally active interleukin or receptor proteins. In principle, many higher eukaryotic tissue culture cell lines are workable, e.g., insect baculovirus expression systems, whether from an invertebrate or vertebrate source. However, mammalian cells are preferred. Transformation or transfection and propagation of such cells has become a routine procedure. Examples of useful cell lines include HeLa cells, Chinese hamster ovary (CHO) cell lines, baby rat kidney (BRK) cell lines, insect cell lines, bird cell lines, and monkey (COS) cell lines. Expression vectors for such cell lines usually include an origin of replication, a promoter, a translation initiation site, RNA splice sites (if genomic DNA is used), a polyadenylation site, and a transcription termination site. These vectors also usually contain a selection gene or amplification gene. Suitable expression vectors may be plasmids, viruses, or retroviruses carrying promoters derived, e.g., from such sources as from adenovirus, SV40, parvoviruses, vaccinia virus, or cytomegalovirus. Representative examples of suitable expression vectors include pCDNA1; pCD, see Okayama, et al. (1985) Mol. Cell Biol. 5:1136-1142; pMC1neo PolyA, see Thomas, et al. (1987) Cell 51:503-512; and a baculovirus vector such as pAC 373 or pAC 610.

For secreted proteins and some membrane proteins, an open reading frame usually encodes a polypeptide that consists of a mature or secreted product covalently linked at its N-terminus to a signal peptide. The signal peptide is cleaved prior to secretion of the mature, or active, polypeptide. The cleavage site can be predicted with a high degree of accuracy from empirical rules, e.g., von-Heijne (1986) Nucleic Acids Research 14:4683-4690 and Nielsen, et al. (1997) Protein Eng. 10:1-12, and the precise amino acid composition of the signal peptide often does not appear to be critical to its function, e.g., Randall, et al. (1989) Science 243:1156-1159; Kaiser et al. (1987) Science 235:312-317. The mature proteins of the invention can be readily determined using standard methods.

It will often be desired to express these polypeptides in a system which provides a specific or defined glycosylation pattern. In this case, the usual pattern will be that provided naturally by the expression system. However, the pattern will
5 be modifiable by exposing the polypeptide, e.g., an unglycosylated form, to appropriate glycosylating proteins introduced into a heterologous expression system. For example, the receptor gene may be co-transformed with one or more genes encoding mammalian or other glycosylating enzymes. Using this
10 approach, certain mammalian glycosylation patterns will be achievable in prokaryote or other cells. Expression in prokaryote cells will typically lead to unglycosylated forms of protein.

The source of DCRS3 or DCRS4 can be a eukaryotic or
15 prokaryotic host expressing recombinant DCRS, such as is described above. The source can also be a cell line, but other mammalian cell lines are also contemplated by this invention, with the preferred cell line being from the human species.

Now that the sequences are known, a primate DCRS3 or DCRS4,
20 fragments, or derivatives thereof can be prepared by conventional processes for synthesizing peptides. These include processes such as are described in Stewart and Young (1984) Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL; Bodanszky and Bodanszky (1984) The Practice of Peptide
25 Synthesis, Springer-Verlag, New York; and Bodanszky (1984) The Principles of Peptide Synthesis, Springer-Verlag, New York; all of each which are incorporated herein by reference. For example, an azide process, an acid chloride process, an acid anhydride process, a mixed anhydride process, an active ester
30 process (for example, p-nitrophenyl ester, N-hydroxysuccinimide ester, or cyanomethyl ester), a carbodiimidazole process, an oxidative-reductive process, or a dicyclohexylcarbodiimide (DCCD)/additive process can be used. Solid phase and solution phase syntheses are both applicable to the foregoing processes.
35 Similar techniques can be used with partial DCRS3 or DCRS4 sequences.

DCRS3 or DCRS4 proteins, fragments, or derivatives are suitably prepared in accordance with the above processes as typically employed in peptide synthesis, generally either by a so-called stepwise process which comprises condensing an amino acid to the terminal amino acid, one by one in sequence, or by coupling peptide fragments to the terminal amino acid. Amino groups that are not being used in the coupling reaction typically must be protected to prevent coupling at an incorrect location.

10 If a solid phase synthesis is adopted, the C-terminal amino acid is bound to an insoluble carrier or support through its carboxyl group. The insoluble carrier is not particularly limited as long as it has a binding capability to a reactive carboxyl group. Examples of such insoluble carriers include 15 halomethyl resins, such as chloromethyl resin or bromomethyl resin, hydroxymethyl resins, phenol resins, tert-alkyloxycarbonylhydrazidated resins, and the like.

An amino group-protected amino acid is bound in sequence through condensation of its activated carboxyl group and the 20 reactive amino group of the previously formed peptide or chain, to synthesize the peptide step by step. After synthesizing the complete sequence, the peptide is split off from the insoluble carrier to produce the peptide. This solid-phase approach is generally described by Merrifield, et al. (1963) in J. Am. Chem. Soc. 85:2149-2156, which is incorporated herein by reference. 25

The prepared protein and fragments thereof can be isolated and purified from the reaction mixture by means of peptide separation, for example, by extraction, precipitation, electrophoresis, various forms of chromatography, and the like. 30 The receptors of this invention can be obtained in varying degrees of purity depending upon desired uses. Purification can be accomplished by use of the protein purification techniques disclosed herein, see below, or by the use of the antibodies herein described in methods of immunoabsorbant affinity 35 chromatography. This immunoabsorbant affinity chromatography is carried out by first linking the antibodies to a solid support and then contacting the linked antibodies with solubilized

lysates of appropriate cells, lysates of other cells expressing the receptor, or lysates or supernatants of cells producing the protein as a result of DNA techniques, see below.

Generally, the purified protein will be at least about 40% pure, ordinarily at least about 50% pure, usually at least about 60% pure, typically at least about 70% pure, more typically at least about 80% pure, preferable at least about 90% pure and more preferably at least about 95% pure, and in particular embodiments, 97%-99% or more. Purity will usually be on a weight basis, but can also be on a molar basis. Different assays will be applied as appropriate. Individual proteins may be purified and thereafter combined.

VI. Antibodies

Antibodies can be raised to various mammalian, e.g., primate DCRS3 or DCRS4 proteins and fragments thereof, both in naturally occurring native forms and in their recombinant forms, the difference being that antibodies to the active receptor are more likely to recognize epitopes which are only present in the native conformations. Denatured antigen detection can also be useful in, e.g., Western analysis. Anti-idiotypic antibodies are also contemplated, which would be useful as agonists or antagonists of a natural receptor or an antibody.

Antibodies, including binding fragments and single chain versions, against predetermined fragments of the protein can be raised by immunization of animals with conjugates of the fragments with immunogenic proteins. Monoclonal antibodies are prepared from cells secreting the desired antibody. These antibodies can be screened for binding to normal or defective protein, or screened for agonistic or antagonistic activity. These monoclonal antibodies will usually bind with at least a K_D of about 1 mM, more usually at least about 300 μ M, typically at least about 100 μ M, more typically at least about 30 μ M, preferably at least about 10 μ M, and more preferably at least about 3 μ M or better.

The antibodies, including antigen binding fragments, of this invention can have significant diagnostic or therapeutic

value. They can be potent antagonists that bind to the receptor and inhibit binding to ligand or inhibit the ability of the receptor to elicit a biological response, e.g., act on its substrate. They also can be useful as non-neutralizing
5 antibodies and can be coupled to toxins or radionuclides to bind producing cells, or cells localized to the source of the interleukin. Further, these antibodies can be conjugated to drugs or other therapeutic agents, either directly or indirectly by means of a linker.

10 The antibodies of this invention can also be useful in diagnostic applications. As capture or non-neutralizing antibodies, they might bind to the receptor without inhibiting ligand or substrate binding. As neutralizing antibodies, they can be useful in competitive binding assays. They will also be
15 useful in detecting or quantifying ligand. They may be used as reagents for Western blot analysis, or for immunoprecipitation or immunopurification of the respective protein. Likewise, nucleic acids and proteins may be immobilized to solid substrates for affinity purification or detection methods. The
20 substrates may be, e.g., solid resin beads or sheets of plastic.

Protein fragments may be joined to other materials, particularly polypeptides, as fused or covalently joined polypeptides to be used as immunogens. Mammalian cytokine receptors and fragments may be fused or covalently linked to a
25 variety of immunogens, such as keyhole limpet hemocyanin, bovine serum albumin, tetanus toxoid, etc. See Microbiology, Hoeber Medical Division, Harper and Row, 1969; Landsteiner (1962) Specificity of Serological Reactions, Dover Publications, New York; and Williams, et al. (1967) Methods in Immunology and
30 Immunochemistry, Vol. 1, Academic Press, New York; each of which are incorporated herein by reference, for descriptions of methods of preparing polyclonal antisera. A typical method involves hyperimmunization of an animal with an antigen. The blood of the animal is then collected shortly after the repeated
35 immunizations and the gamma globulin is isolated.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents,

primates, humans, etc. Description of techniques for preparing such monoclonal antibodies may be found in, e.g., Stites, et al. (eds.) Basic and Clinical Immunology (4th ed.), Lange Medical Publications, Los Altos, CA, and references cited therein;

5 Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press, New York; and particularly in Kohler and Milstein (1975) in Nature 256: 495-497, which discusses one method of generating monoclonal antibodies. Each

10 of these references is incorporated herein by reference. Summarized briefly, this method involves injecting an animal with an immunogen. The animal is then sacrificed and cells taken from its spleen, which are then fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of

15 reproducing in vitro. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal

20 generated in response to a specific site recognized on the immunogenic substance.

Other suitable techniques involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar

25 vectors. See, Huse, et al. (1989) "Generation of a Large Combinatorial Library of the Immunoglobulin Repertoire in Phage Lambda," Science 246:1275-1281; and Ward, et al. (1989) Nature 341:544-546, each of which is hereby incorporated herein by reference. The polypeptides and antibodies of the present

30 invention may be used with or without modification, including chimeric or humanized antibodies. Frequently, the polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are

35 known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent

moieties, chemiluminescent moieties, magnetic particles, and the like. Patents, teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant or
5 chimeric immunoglobulins may be produced, see Cabilly, U.S. Patent No. 4,816,567; or made in transgenic mice, see Mendez, et al. (1997) Nature Genetics 15:146-156. These references are incorporated herein by reference.

The antibodies of this invention can also be used for
10 affinity chromatography in isolating DCRS3 proteins or peptides. Columns can be prepared where the antibodies are linked to a solid support, e.g., particles, such as agarose, Sephadex, or the like, where a cell lysate may be passed through the column, the column washed, followed by increasing concentrations of a
15 mild denaturant, whereby the purified protein will be released. Alternatively, the protein may be used to purify antibody. Appropriate cross absorptions or depletions may be applied.

The antibodies may also be used to screen expression libraries for particular expression products. Usually the
20 antibodies used in such a procedure will be labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

Antibodies raised against a cytokine receptor will also be used to raise anti-idiotypic antibodies. These will be useful
25 in detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein. They also will be useful as agonists or antagonists of the ligand, which may be competitive inhibitors or substitutes for naturally occurring ligands.

30 A cytokine receptor protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NO: 2, 25, 5, 28, or 31, is typically determined in an immunoassay. The immunoassay
35 typically uses a polyclonal antiserum which was raised, e.g., to a protein of SEQ ID NO: 2, 25, 5, 28, or 31. This antiserum is selected to have low crossreactivity against other cytokine

receptor family members, e.g., IL-11 receptor subunit alpha, IL-6 receptor subunit alpha, or p40, preferably from the same species, and any such crossreactivity is removed by immunoabsorption prior to use in the immunoassay.

- 5 In order to produce antisera for use in an immunoassay, the protein, e.g., of SEQ ID NO: 2, 25, 5, 28, or 31, is isolated as described herein. For example, recombinant protein may be produced in a mammalian cell line. An appropriate host, e.g., an inbred strain of mice such as Balb/c, is immunized with the
10 selected protein, typically using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, supra). Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen.
- 15 Polyclonal sera are collected and titered against the immunogen protein in an immunoassay, e.g., a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against other cytokine receptor
20 family members, e.g., IL-2, IL-7, IL-9, or EPO receptor subunit, using a competitive binding immunoassay such as the one described in Harlow and Lane, supra, at pages 570-573. Preferably at least two cytokine receptor family members are used in this determination. These cytokine receptor family
25 members can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

- Immunoassays in the competitive binding format can be used for the crossreactivity determinations. For example, the
30 protein of SEQ ID NO: 2, 25, 5, 28, or 31 can be immobilized to a solid support. Proteins added to the assay compete with the binding of the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the proteins,
35 e.g., of IL-2, IL-7, IL-9, or EPO receptor subunit. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10%

crossreactivity with each of the proteins listed above are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorption with the above-listed proteins.

5 The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein to the immunogen protein (e.g., DCRS3 like protein of SEQ ID NO: 2). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations
10 and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required is less than twice the amount of the protein of the selected protein or proteins that is required, then the second protein is
15 said to specifically bind to an antibody generated to the immunogen.

It is understood that these cytokine receptor proteins are members of a family of homologous proteins that comprise at least 6 so far identified genes. For a particular gene product,
20 such as a DCRS3 or DCRS4, the term refers not only to the amino acid sequences disclosed herein, but also to other proteins that are allelic, non-allelic, or species variants. It is also understood that the terms include nonnatural mutations introduced by deliberate mutation using conventional recombinant
25 technology such as single site mutation, or by excising short sections of DNA encoding the respective proteins, or by substituting new amino acids, or adding new amino acids. Such minor alterations typically will substantially maintain the immunoidentity of the original molecule and/or its biological
30 activity. Thus, these alterations include proteins that are specifically immunoreactive with a designated naturally occurring DCRS3 or DCRS4 protein. The biological properties of the altered proteins can be determined by expressing the protein in an appropriate cell line and measuring the appropriate
35 effect, e.g., upon transfected lymphocytes. Particular protein modifications considered minor would include conservative substitution of amino acids with similar chemical properties, as

described above for the cytokine receptor family as a whole. By aligning a protein optimally with the protein of the cytokine receptors and by using the conventional immunoassays described herein to determine immunoidentity, one can determine the protein compositions of the invention.

VII. Kits and quantitation

Both naturally occurring and recombinant forms of the cytokine receptor like molecules of this invention are particularly useful in kits and assay methods. For example, these methods would also be applied to screening for binding activity, e.g., ligands for these proteins. Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds per year. See, e.g., a BIOMEK automated workstation, Beckman Instruments, Palo Alto, California, and Fodor, et al. (1991) Science 251:767-773, which is incorporated herein by reference. The latter describes means for testing binding by a plurality of defined polymers synthesized on a solid substrate. The development of suitable assays to screen for a ligand or agonist/antagonist homologous proteins can be greatly facilitated by the availability of large amounts of purified, soluble cytokine receptors in an active state such as is provided by this invention.

Purified DCRS3 or DCRS4 can be coated directly onto plates for use in the aforementioned ligand screening techniques. However, non-neutralizing antibodies to these proteins can be used as capture antibodies to immobilize the respective receptor on the solid phase, useful, e.g., in diagnostic uses.

This invention also contemplates use of DCRS3 or DCRS4, fragments thereof, peptides, and their fusion products in a variety of diagnostic kits and methods for detecting the presence of the protein or its ligand. Alternatively, or additionally, antibodies against the molecules may be incorporated into the kits and methods. Typically the kit will have a compartment containing either a DCRS3 or DCRS4 peptide or gene segment or a reagent which recognizes one or the other.

Typically, recognition reagents, in the case of peptide, would be a receptor or antibody, or in the case of a gene segment, would usually be a hybridization probe.

A preferred kit for determining the concentration of, e.g., DCRS3 in a sample would typically comprise a labeled compound, e.g., ligand or antibody, having known binding affinity for DCRS3, a source of DCRS3 (naturally occurring or recombinant) as a positive control, and a means for separating the bound from free labeled compound, for example a solid phase for immobilizing DCRS3 in the test sample. Compartments containing reagents, and instructions, will normally be provided. Appropriate nucleic acid or protein containing kits are also provided.

Antibodies, including antigen binding fragments, specific for mammalian DCRS3 or a peptide fragment, or receptor fragments are useful in diagnostic applications to detect the presence of elevated levels of ligand and/or its fragments. Diagnostic assays may be homogeneous (without a separation step between free reagent and antibody-antigen complex) or heterogeneous (with a separation step). Various commercial assays exist, such as radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), enzyme-multiplied immunoassay technique (EMIT), substrate-labeled fluorescent immunoassay (SLFIA) and the like. For example, unlabeled antibodies can be employed by using a second antibody which is labeled and which recognizes the antibody to a cytokine receptor or to a particular fragment thereof. These assays have also been extensively discussed in the literature. See, e.g., Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH., and Coligan (ed. 1991 and periodic supplements) Current Protocols In Immunology Greene/Wiley, New York.

Anti-idiotypic antibodies may have similar use to serve as agonists or antagonists of cytokine receptors. These should be useful as therapeutic reagents under appropriate circumstances.

Frequently, the reagents for diagnostic assays are supplied in kits, so as to optimize the sensitivity of the assay. For the subject invention, depending upon the nature of the assay,

the protocol, and the label, either labeled or unlabeled antibody, or labeled ligand is provided. This is usually in conjunction with other additives, such as buffers, stabilizers, materials necessary for signal production such as substrates for enzymes, and the like. Preferably, the kit will also contain instructions for proper use and disposal of the contents after use. Typically the kit has compartments for each useful reagent, and will contain instructions for proper use and disposal of reagents. Desirably, the reagents are provided as a dry lyophilized powder, where the reagents may be reconstituted in an aqueous medium having appropriate concentrations for performing the assay.

The aforementioned constituents of the diagnostic assays may be used without modification or may be modified in a variety of ways. For example, labeling may be achieved by covalently or non-covalently joining a moiety which directly or indirectly provides a detectable signal. In many of these assays, a test compound, cytokine receptor, or antibodies thereto can be labeled either directly or indirectly. Possibilities for direct labeling include label groups: radiolabels such as ^{125}I , enzymes (U.S. Pat. No. 3,645,090) such as peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) capable of monitoring the change in fluorescence intensity, wavelength shift, or fluorescence polarization. Both of the patents are incorporated herein by reference. Possibilities for indirect labeling include biotinylation of one constituent followed by binding to avidin coupled to one of the above label groups.

There are also numerous methods of separating the bound from the free ligand, or alternatively the bound from the free test compound. The cytokine receptor can be immobilized on various matrixes followed by washing. Suitable matrices include plastic such as an ELISA plate, filters, and beads. Methods of immobilizing the receptor to a matrix include, without limitation, direct adhesion to plastic, use of a capture antibody, chemical coupling, and biotin-avidin. The last step in this approach involves the precipitation of antibody/antigen

complex by any of several methods including those utilizing, e.g., an organic solvent such as polyethylene glycol or a salt such as ammonium sulfate. Other suitable separation techniques include, without limitation, the fluorescein antibody

5 magnetizable particle method described in Rattle, et al. (1984) Clin. Chem. 30:1457-1461, and the double antibody magnetic particle separation as described in U.S. Pat. No. 4,659,678, each of which is incorporated herein by reference.

The methods for linking protein or fragments to various
10 labels have been extensively reported in the literature and do not require detailed discussion here. Many of the techniques involve the use of activated carboxyl groups either through the use of carbodiimide or active esters to form peptide bonds, the formation of thioethers by reaction of a mercapto group with an
15 activated halogen such as chloroacetyl, or an activated olefin such as maleimide, for linkage, or the like. Fusion proteins will also find use in these applications.

Another diagnostic aspect of this invention involves use of oligonucleotide or polynucleotide sequences taken from the
20 sequence of an cytokine receptor. These sequences can be used as probes for detecting levels of the respective cytokine receptor in patients suspected of having an immunological disorder. The preparation of both RNA and DNA nucleotide sequences, the labeling of the sequences, and the preferred size
25 of the sequences has received ample description and discussion in the literature. Normally an oligonucleotide probe should have at least about 14 nucleotides, usually at least about 18 nucleotides, and the polynucleotide probes may be up to several kilobases. Various labels may be employed, most commonly
30 radionuclides, particularly ^{32}P . However, other techniques may also be employed, such as using biotin modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides,
35 fluorescers, enzymes, or the like. Alternatively, antibodies may be employed which can recognize specific duplexes, including DNA duplexes, RNA duplexes, DNA-RNA hybrid duplexes, or

DNA-protein duplexes. The antibodies in turn may be labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected. The use of probes to the novel anti-sense RNA may be carried out in conventional techniques such as nucleic acid hybridization, plus and minus screening, recombinational probing, hybrid released translation (HRT), and hybrid arrested translation (HART). This also includes amplification techniques such as polymerase chain reaction (PCR).

Diagnostic kits which also test for the qualitative or quantitative presence of other markers are also contemplated. Diagnosis or prognosis may depend on the combination of multiple indications used as markers. Thus, kits may test for combinations of markers. See, e.g., Viallet, et al. (1989) Progress in Growth Factor Res. 1:89-97.

VIII. Therapeutic Utility

This invention provides reagents with significant therapeutic value. See, e.g., Levitzki (1996) Curr. Opin. Cell Biol. 8:239-244. The cytokine receptors (naturally occurring or recombinant), fragments thereof, mutein receptors, and antibodies, along with compounds identified as having binding affinity to the receptors or antibodies, should be useful in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. Such abnormality will typically be manifested by immunological disorders. Additionally, this invention should provide therapeutic value in various diseases or disorders associated with abnormal expression or abnormal triggering of response to the ligand. For example, the IL-1 ligands have been suggested to be involved in morphologic development, e.g., dorso-ventral polarity determination, and immune responses, particularly the primitive innate responses. See, e.g., Sun, et al. (1991) Eur. J. Biochem. 196:247-254; and Hultmark (1994) Nature 367:116-117.

Recombinant cytokine receptors, muteins, agonist or antagonist antibodies thereto, or antibodies can be purified and

then administered to a patient. These reagents can be combined for therapeutic use with additional active ingredients, e.g., in conventional pharmaceutically acceptable carriers or diluents, along with physiologically innocuous stabilizers and excipients. These combinations can be sterile, e.g., filtered, and placed into dosage forms as by lyophilization in dosage vials or storage in stabilized aqueous preparations. This invention also contemplates use of antibodies or binding fragments thereof which are not complement binding.

10 Ligand screening using cytokine receptor or fragments thereof can be performed to identify molecules having binding affinity to the receptors. Subsequent biological assays can then be utilized to determine if a putative ligand can provide competitive binding, which can block intrinsic stimulating activity. Receptor fragments can be used as a blocker or antagonist in that it blocks the activity of ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of ligand, e.g., inducing signaling. This invention further contemplates the therapeutic use of antibodies to cytokine receptors as antagonists.

The quantities of reagents necessary for effective therapy will depend upon many different factors, including means of administration, target site, reagent physiological life, pharmacological life, physiological state of the patient, and other medicants administered. Thus, treatment dosages should be titrated to optimize safety and efficacy. Typically, dosages used in vitro may provide useful guidance in the amounts useful for in situ administration of these reagents. Animal testing of effective doses for treatment of particular disorders will provide further predictive indication of human dosage. Various considerations are described, e.g., in Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; each of which is hereby incorporated herein by reference. Methods for administration are discussed therein and

below, e.g., for oral, intravenous, intraperitoneal, or intramuscular administration, transdermal diffusion, and others. Pharmaceutically acceptable carriers will include water, saline, buffers, and other compounds described, e.g., in the Merck Index, Merck & Co., Rahway, New Jersey. Because of the likely high affinity binding, or turnover numbers, between a putative ligand and its receptors, low dosages of these reagents would be initially expected to be effective. And the signaling pathway suggests extremely low amounts of ligand may have effect. Thus, dosage ranges would ordinarily be expected to be in amounts lower than 1 mM concentrations, typically less than about 10 μ M concentrations, usually less than about 100 nM, preferably less than about 10 pM (picomolar), and most preferably less than about 1 fM (femtomolar), with an appropriate carrier. Slow release formulations, or slow release apparatus will often be utilized for continuous administration.

Cytokine receptors, fragments thereof, and antibodies or its fragments, antagonists, and agonists, may be administered directly to the host to be treated or, depending on the size of the compounds, it may be desirable to conjugate them to carrier proteins such as ovalbumin or serum albumin prior to their administration. Therapeutic formulations may be administered in many conventional dosage formulations. While it is possible for the active ingredient to be administered alone, it is preferable to present it as a pharmaceutical formulation. Formulations comprise at least one active ingredient, as defined above, together with one or more acceptable carriers thereof. Each carrier must be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. Formulations include those suitable for oral, rectal, nasal, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by methods well known in the art of pharmacy. See, e.g., Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's

Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; Avis, et al. (eds. 1993) Pharmaceutical Dosage Forms: Parenteral Medications Dekker, NY; Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Tablets Dekker, NY; and
5 Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Disperse Systems Dekker, NY. The therapy of this invention may be combined with or used in association with other therapeutic agents, particularly agonists or antagonists of other cytokine receptor family members.

10

IX. Screening

Drug screening using DCRS3 or DCRS4 or fragments thereof can be performed to identify compounds having binding affinity to the receptor subunit, including isolation of associated
15 components. Subsequent biological assays can then be utilized to determine if the compound has intrinsic stimulating activity and is therefore a blocker or antagonist in that it blocks the activity of the ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an
20 agonist in that it simulates the activity of a cytokine ligand. This invention further contemplates the therapeutic use of antibodies to the receptor as cytokine agonists or antagonists.

Similarly, complexes comprising multiple proteins may be used to screen for ligands or reagents capable of recognizing
25 the complex. Most cytokine receptors comprise at least two subunits, which may be the same, or distinct. Alternatively, the transmembrane receptor may bind to a complex comprising a cytokine-like ligand associated with another soluble protein serving, e.g., as a second receptor subunit.

30 One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant DNA molecules expressing, e.g., a DCRS3 in combination with another cytokine receptor subunit. Cells may be isolated which express a receptor in isolation from other
35 functional receptors. Such cells, either in viable or fixed form, can be used for standard antibody/antigen or ligand/receptor binding assays. See also, Parce, et al. (1989) Science 246:243-247; and Owicki, et al. (1990) Proc. Nat'l Acad.

Sci. USA 87:4007-4011, which describe sensitive methods to detect cellular responses. Competitive assays are particularly useful, where the cells (source of putative ligand) are contacted and incubated with a labeled receptor or antibody having known binding affinity to the ligand, such as ^{125}I -antibody, and a test sample whose binding affinity to the binding composition is being measured. The bound and free labeled binding compositions are then separated to assess the degree of ligand binding. The amount of test compound bound is inversely proportional to the amount of labeled receptor binding to the known source. Many techniques can be used to separate bound from free ligand to assess the degree of ligand binding. This separation step could typically involve a procedure such as adhesion to filters followed by washing, adhesion to plastic followed by washing, or centrifugation of the cell membranes. Viable cells could also be used to screen for the effects of drugs on cytokine mediated functions, e.g., second messenger levels, i.e., Ca^{++} ; cell proliferation; inositol phosphate pool changes; and others. Some detection methods allow for elimination of a separation step, e.g., a proximity sensitive detection system. Calcium sensitive dyes will be useful for detecting Ca^{++} levels, with a fluorimeter or a fluorescence cell sorting apparatus.

25 X. Ligands

The descriptions of DCRS3 or DCRS4 herein provide means to identify ligands, as described above. Such ligand should bind specifically to the respective receptor with reasonably high affinity. Various constructs are made available which allow either labeling of the receptor to detect its ligand. For example, directly labeling cytokine receptor, fusing onto it markers for secondary labeling, e.g., FLAG or other epitope tags, etc., will allow detection of receptor. This can be histological, as an affinity method for biochemical purification, or labeling or selection in an expression cloning approach. A two-hybrid selection system may also be applied making appropriate constructs with the available cytokine

receptor sequences. See, e.g., Fields and Song (1989) Nature 340:245-246.

The broad scope of this invention is best understood with reference to the following examples, which are not intended to
5 limit the inventions to the specific embodiments.

EXAMPLES

I. General Methods

10 Some of the standard methods are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; or Ausubel, et al. (1987 and
15 Supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York. Methods for protein purification include such methods as ammonium sulfate precipitation, column chromatography, electrophoresis, centrifugation, crystallization, and others. See, e.g., Ausubel, et al. (1987
20 and periodic supplements); Coligan, et al. (ed. 1996) and periodic supplements, Current Protocols In Protein Science Greene/Wiley, New York; Deutscher (1990) "Guide to Protein Purification" in Methods in Enzymology, vol. 182, and other volumes in this series; and manufacturer's literature on use of
25 protein purification products, e.g., Pharmacia, Piscataway, N.J., or Bio-Rad, Richmond, CA. Combination with recombinant techniques allow fusion to appropriate segments, e.g., to a FLAG sequence or an equivalent which can be fused via a protease-removable sequence. See, e.g., Hochuli (1990) "Purification of
30 Recombinant Proteins with Metal Chelate Absorbent" in Setlow (ed.) Genetic Engineering, Principle and Methods 12:87-98, Plenum Press, N.Y.; and Crowe, et al. (1992) QIAexpress: The High Level Expression & Protein Purification System QUIAGEN, Inc., Chatsworth, CA.

35 Computer sequence analysis is performed, e.g., using available software programs, including those from the GCG (U. Wisconsin) and GenBank sources. Public sequence databases were also used, e.g., from GenBank and others.

Many techniques applicable to IL-10 receptors may be applied to DCRS3 or DCRS4, as described, e.g., in USSN 08/110,683 (IL-10 receptor), which is incorporated herein by reference.

II. Computational Analysis

Human sequences related to cytokine receptors were identified from genomic sequence database using, e.g., the BLAST server (Altschul, et al. (1994) Nature Genet. 6:119-129). Standard analysis programs may be used to evaluate structure, e.g., PHD (Rost and Sander (1994) Proteins 19:55-72) and DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310). Standard comparison software includes, e.g., Altschul, et al. (1990) J. Mol. Biol. 215:403-10; Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chapman & Hall; Lander and Waterman (eds. 1995) Calculating the Secrets of Life: Applications of the Mathematical Sciences in Molecular Biology National Academy Press; and Speed and Waterman (eds. 1996) Genetic Mapping and DNA Sequencing (IMA Volumes in Mathematics and Its Applications, Vol 81) Springer Verlag.

III. Cloning of full-length DCRS3 or DCRS4 cDNAs; Chromosomal localization

PCR primers derived from DCRS3 or DCRS4 sequence are used to probe a human cDNA library. Sequences may be derived, e.g., from Table 1 or 3, preferably those adjacent the ends of sequences. Full length cDNAs for primate, rodent, or other species are cloned, e.g., by DNA hybridization screening of λ gt10 phage. PCR reactions are conducted using T. aquaticus Taqplus DNA polymerase (Stratagene) under appropriate conditions.

For experimental confirmation of localization, chromosome spreads are prepared. In situ hybridization is performed on chromosome preparations obtained from phytohemagglutinin-stimulated human lymphocytes cultured for 72 h. 5-bromodeoxyuridine was added for the final seven hours of culture (60 μ g/ml of medium), to ensure a posthybridization chromosomal banding of good quality.

A PCR fragment, amplified with the help of primers, is cloned into an appropriate vector. The vector is labeled by nick-translation with ^3H . The radiolabeled probe is hybridized to metaphase spreads at final concentration of 200 ng/ml of

hybridization solution as described in Mattei, et al. (1985) Hum. Genet. 69:327-331.

After coating with nuclear track emulsion (KODAK NTB₂), slides are exposed. To avoid any slipping of silver grains during the banding procedure, chromosome spreads are first stained with buffered Giemsa solution and metaphase photographed. R-banding is then performed by the fluorochrome-photolysis-Giemsa (FPG) method and metaphases rephotographed before analysis.

10 Similar appropriate methods are used for other species.

IV. Localization of DCRS mRNA

Human multiple tissue (Cat# 1, 2) and cancer cell line blots (Cat# 7757-1), containing approximately 2 µg of poly(A)⁺ RNA per lane, are purchased from Clontech (Palo Alto, CA). Probes are radiolabeled with [α -³²P] dATP, e.g., using the Amersham Rediprime random primer labeling kit (RPN1633). Prehybridization and hybridizations are performed, e.g., at 65° C in 0.5 M Na₂HPO₄, 7% SDS, 0.5 M EDTA (pH 8.0). High stringency washes are conducted, e.g., at 65° C with two initial washes in 2 x SSC, 0.1% SDS for 40 min followed by a subsequent wash in 0.1 x SSC, 0.1% SDS for 20 min. Membranes are then exposed at -70° C to X-Ray film (Kodak) in the presence of intensifying screens. More detailed studies by cDNA library Southern are performed with selected appropriate human DCRS3 clones to examine their expression in hemopoietic or other cell subsets.

Alternatively, two appropriate primers are selected from Tables 1 or 3. RT-PCR is used on an appropriate mRNA sample selected for the presence of message to produce a cDNA, e.g., a sample which expresses the gene.

Full length clones may be isolated by hybridization of cDNA libraries from appropriate tissues pre-selected by PCR signal. Northern blots can be performed.

35 Message for genes encoding DCRS3 or DCRS4 will be assayed by appropriate technology, e.g., PCR, immunoassay, hybridization, or otherwise. Tissue and organ cDNA preparations

are available, e.g., from Clontech, Mountain View, CA.

Identification of sources of natural expression are useful, as described. And the identification of functional receptor subunit pairings will allow for prediction of what cells express the combination of receptor subunits which will result in a physiological responsiveness to each of the cytokine ligands.

For mouse distribution, e.g., Southern Analysis can be performed: DNA (5 µg) from a primary amplified cDNA library was digested with appropriate restriction enzymes to release the inserts, run on a 1% agarose gel and transferred to a nylon membrane (Schleicher and Schuell, Keene, NH).

Samples for mouse mRNA isolation may include: resting mouse fibroblastic L cell line (C200); Braf:ER (Braf fusion to estrogen receptor) transfected cells, control (C201); T cells, TH1 polarized (Mell14 bright, CD4+ cells from spleen, polarized for 7 days with IFN-γ and anti IL-4; T200); T cells, TH2 polarized (Mell14 bright, CD4+ cells from spleen, polarized for 7 days with IL-4 and anti-IFN-γ; T201); T cells, highly TH1 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T202); T cells, highly TH2 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T203); CD44- CD25+ pre T cells, sorted from thymus (T204); TH1 T cell clone D1.1, resting for 3 weeks after last stimulation with antigen (T205); TH1 T cell clone D1.1, 10 µg/ml ConA stimulated 15 h (T206); TH2 T cell clone CDC35, resting for 3 weeks after last stimulation with antigen (T207); TH2 T cell clone CDC35, 10 µg/ml ConA stimulated 15 h (T208); Mell14+ naive T cells from spleen, resting (T209); Mell14+ T cells, polarized to Th1 with IFN-γ/IL-12/anti-IL-4 for 6, 12, 24 h pooled (T210); Mell14+ T cells, polarized to Th2 with IL-4/anti-IFN-γ for 6, 13, 24 h pooled (T211); unstimulated mature B cell leukemia cell line A20 (B200); unstimulated B cell line CH12 (B201); unstimulated large B cells from spleen (B202); B cells from total spleen, LPS activated (B203); metrizamide enriched dendritic cells from spleen, resting (D200); dendritic cells from bone marrow, resting (D201); monocyte cell line RAW 264.7

activated with LPS 4 h (M200); bone-marrow macrophages derived
 with GM and M-CSF (M201); macrophage cell line J774, resting
 (M202); macrophage cell line J774 + LPS + anti-IL-10 at 0.5, 1,
 3, 6, 12 h pooled (M203); macrophage cell line J774 + LPS + IL-
 5 10 at 0.5, 1, 3, 5, 12 h pooled (M204); aerosol challenged mouse
 lung tissue, Th2 primers, aerosol OVA challenge 7, 14, 23 h
 pooled (see Garlisi, et al. (1995) Clinical Immunology and
Immunopathology 75:75-83; X206); Nippostrongylus-infected lung
 tissue (see Coffman, et al. (1989) Science 245:308-310; X200);
 10 total adult lung, normal (O200); total lung, rag-1 (see Schwarz,
 et al. (1993) Immunodeficiency 4:249-252; O205); IL-10 K.O.
 spleen (see Kuhn, et al. (1991) Cell 75:263-274; X201); total
 adult spleen, normal (O201); total spleen, rag-1 (O207); IL-10
 K.O. Peyer's patches (O202); total Peyer's patches, normal
 15 (O210); IL-10 K.O. mesenteric lymph nodes (X203); total
 mesenteric lymph nodes, normal (O211); IL-10 K.O. colon (X203);
 total colon, normal (O212); NOD mouse pancreas (see Makino, et
 al. (1980) Jikken Dobutsu 29:1-13; X205); total thymus, rag-1
 (O208); total kidney, rag-1 (O209); total heart, rag-1 (O202);
 20 total brain, rag-1 (O203); total testes, rag-1 (O204); total
 liver, rag-1 (O206); rat normal joint tissue (O300); and rat
 arthritic joint tissue (X300).

Samples for human mRNA isolation may include: peripheral
 blood mononuclear cells (monocytes, T cells, NK cells,
 25 granulocytes, B cells), resting (T100); peripheral blood
 mononuclear cells, activated with anti-CD3 for 2, 6, 12 h pooled
 (T101); T cell, TH0 clone Mot 72, resting (T102); T cell, TH0
 clone Mot 72, activated with anti-CD28 and anti-CD3 for 3, 6, 12
 h pooled (T103); T cell, TH0 clone Mot 72, anergic treated with
 30 specific peptide for 2, 7, 12 h pooled (T104); T cell, TH1 clone
 HY06, resting (T107); T cell, TH1 clone HY06, activated with
 anti-CD28 and anti-CD3 for 3, 6, 12 h pooled (T108); T cell, TH1
 clone HY06, anergic treated with specific peptide for 2, 6, 12 h
 pooled (T109); T cell, TH2 clone HY935, resting (T110); T cell,
 35 TH2 clone HY935, activated with anti-CD28 and anti-CD3 for 2, 7,
 12 h pooled (T111); T cells CD4+CD45RO- T cells polarized 27
 days in anti-CD28, IL-4, and anti IFN- γ , TH2 polarized, activated

with anti-CD3 and anti-CD28 4 h (T116); T cell tumor lines Jurkat and Hut78, resting (T117); T cell clones, pooled AD130.2, Tc783.12, Tc783.13, Tc783.58, Tc782.69, resting (T118); T cell random $\gamma\delta$ T cell clones, resting (T119); Splenocytes, resting (B100); Splenocytes, activated with anti-CD40 and IL-4 (B101); B cell EBV lines pooled WT49, RSB, JY, CVIR, 721.221, RM3, HSY, resting (B102); B cell line JY, activated with PMA and ionomycin for 1, 6 h pooled (B103); NK 20 clones pooled, resting (K100); NK 20 clones pooled, activated with PMA and ionomycin for 6 h (K101); NKL clone, derived from peripheral blood of LGL leukemia patient, IL-2 treated (K106); NK cytotoxic clone 640-A30-1, resting (K107); hematopoietic precursor line TF1, activated with PMA and ionomycin for 1, 6 h pooled (C100); U937 premonocytic line, resting (M100); U937 premonocytic line, activated with PMA and ionomycin for 1, 6 h pooled (M101); elutriated monocytes, activated with LPS, IFN γ , anti-IL-10 for 1, 2, 6, 12, 24 h pooled (M102); elutriated monocytes, activated with LPS, IFN γ , IL-10 for 1, 2, 6, 12, 24 h pooled (M103); elutriated monocytes, activated with LPS, IFN γ , anti-IL-10 for 4, 16 h pooled (M106); elutriated monocytes, activated with LPS, IFN γ , IL-10 for 4, 16 h pooled (M107); elutriated monocytes, activated LPS for 1 h (M108); elutriated monocytes, activated LPS for 6 h (M109); DC 70% CD1a+, from CD34+ GM-CSF, TNF α 12 days, resting (D101); DC 70% CD1a+, from CD34+ GM-CSF, TNF α 12 days, activated with PMA and ionomycin for 1 hr (D102); DC 70% CD1a+, from CD34+ GM-CSF, TNF α 12 days, activated with PMA and ionomycin for 6 hr (D103); DC 95% CD1a+, from CD34+ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and ionomycin for 1, 6 h pooled (D104); DC 95% CD14+, ex CD34+ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and ionomycin 1, 6 hr pooled (D105); DC CD1a+ CD86+, from CD34+ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and ionomycin for 1, 6 h pooled (D106); DC from monocytes GM-CSF, IL-4 5 days, resting (D107); DC from monocytes GM-CSF, IL-4 5 days, resting (D108); DC from monocytes GM-CSF, IL-4 5 days, activated LPS 4, 16 h pooled (D109); DC from monocytes GM-CSF, IL-4 5 days, activated TNF α , monocyte supe for 4, 16 h pooled (D110); leiomyoma L11 benign tumor (X101); normal myometrium M5

(O115); malignant leiomyosarcoma GS1 (X103); lung fibroblast sarcoma line MRC5, activated with PMA and ionomycin for 1, 6 h pooled (C101); kidney epithelial carcinoma cell line CHA, activated with PMA and ionomycin for 1, 6 h pooled (C102);
5 kidney fetal 28 wk male (O100); lung fetal 28 wk male (O101); liver fetal 28 wk male (O102); heart fetal 28 wk male (O103); brain fetal 28 wk male (O104); gallbladder fetal 28 wk male (O106); small intestine fetal 28 wk male (O107); adipose tissue fetal 28 wk male (O108); ovary fetal 25 wk female (O109); uterus
10 fetal 25 wk female (O110); testes fetal 28 wk male (O111); spleen fetal 28 wk male (O112); adult placenta 28 wk (O113); and tonsil inflamed, from 12 year old (X100).

Similar samples may isolated in other species for evaluation.

15

V. Cloning of species counterparts of DCRS3 or DCRS4

Various strategies are used to obtain species counterparts of DCRS3 or DCRS4, preferably from other primates or rodents. One method is by cross hybridization using closely related
20 species DNA probes. It may be useful to go into evolutionarily similar species as intermediate steps. Another method is by using specific PCR primers based on the identification of blocks of similarity or difference between genes, e.g., areas of highly conserved or nonconserved polypeptide or nucleotide sequence.
25 Antibody based screening methods are also available, e.g., in expression cloning.

VI. Production of mammalian DCRS3 or DCRS4 protein

An appropriate, e.g., GST, fusion construct is engineered
30 for expression, e.g., in E. coli. For example, a mouse IGIF pGex plasmid is constructed and transformed into E. coli. Freshly transformed cells are grown, e.g., in LB medium containing 50 µg/ml ampicillin and induced with IPTG (Sigma, St. Louis, MO). After overnight induction, the bacteria are
35 harvested and the pellets containing, e.g., DCRS3, protein are isolated. The pellets are homogenized, e.g., in TE buffer (50 mM Tris-base pH 8.0, 10 mM EDTA and 2 mM pefabloc) in 2 liters.

This material is passed through a microfluidizer (Microfluidics, Newton, MA) three times. The fluidized supernatant is spun down on a Sorvall GS-3 rotor for 1 h at 13,000 rpm. The resulting supernatant containing the cytokine receptor protein is filtered and passed over a glutathione-SEPHAROSE column equilibrated in 50 mM Tris-base pH 8.0. The fractions containing the DCRS3-GST fusion protein are pooled and cleaved, e.g., with thrombin (Enzyme Research Laboratories, Inc., South Bend, IN). The cleaved pool is then passed over a Q-SEPHAROSE column equilibrated in 50 mM Tris-base. Fractions containing DCRS3 are pooled and diluted in cold distilled H₂O, to lower the conductivity, and passed back over a fresh Q-Sepharose column, alone or in succession with an immunoaffinity antibody column. Fractions containing DCRS3 protein are pooled, aliquoted, and stored in the -70° C freezer.

Comparison of the CD spectrum with cytokine receptor protein may suggest that the protein is correctly folded. See Hazuda, et al. (1969) J. Biol. Chem. 264:1689-1693.

VII. Preparation of antibodies specific for DCRS3 or DCRS4

Inbred Balb/c mice are immunized intraperitoneally with recombinant forms of the protein, e.g., purified DCRS3 or stable transfected NIH-3T3 cells. Animals are boosted at appropriate time points with protein, with or without additional adjuvant, to further stimulate antibody production. Serum is collected, or hybridomas produced with harvested spleens.

Alternatively, Balb/c mice are immunized with cells transformed with the gene or fragments thereof, either endogenous or exogenous cells, or with isolated membranes enriched for expression of the antigen. Serum is collected at the appropriate time, typically after numerous further administrations. Various gene therapy techniques may be useful, e.g., in producing protein in situ, for generating an immune response. Serum or antibody preparations may be cross-absorbed or immunoselected to prepare substantially purified antibodies of defined specificity and high affinity.

Monoclonal antibodies may be made. For example, splenocytes are fused with an appropriate fusion partner and hybridomas are selected in growth medium by standard procedures. Hybridoma supernatants are screened for the presence of antibodies which bind to DCRS3, e.g., by ELISA or other assay. Antibodies which specifically recognize specific DCRS3 embodiments may also be selected or prepared.

In another method, synthetic peptides or purified protein are presented to an immune system to generate monoclonal or polyclonal antibodies. See, e.g., Coligan (ed. 1991) Current Protocols in Immunology Wiley/Greene; and Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press. In appropriate situations, the binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods. Nucleic acids may also be introduced into cells in an animal to produce the antigen, which serves to elicit an immune response. See, e.g., Wang, et al. (1993) Proc. Nat'l. Acad. Sci. 90:4156-4160; Barry, et al. (1994) BioTechniques 16:616-619; and Xiang, et al. (1995) Immunity 2: 129-135.

VIII. Production of fusion proteins with DCRS

Various fusion constructs are made with DCRS. A portion of the appropriate gene is fused to an epitope tag, e.g., a FLAG tag, or to a two hybrid system construct. See, e.g., Fields and Song (1989) Nature 340:245-246.

The epitope tag may be used in an expression cloning procedure with detection with anti-FLAG antibodies to detect a binding partner, e.g., ligand for the respective cytokine receptor. The two hybrid system may also be used to isolate proteins which specifically bind to DCRS.

IX. Structure activity relationship

Information on the criticality of particular residues is determined using standard procedures and analysis. Standard mutagenesis analysis is performed, e.g., by generating many different variants at determined positions, e.g., at the

positions identified above, and evaluating biological activities of the variants. This may be performed to the extent of determining positions which modify activity, or to focus on specific positions to determine the residues which can be substituted to either retain, block, or modulate biological activity.

Alternatively, analysis of natural variants can indicate what positions tolerate natural mutations. This may result from populational analysis of variation among individuals, or across strains or species. Samples from selected individuals are analyzed, e.g., by PCR analysis and sequencing. This allows evaluation of population polymorphisms.

X. Isolation of a ligand for DCRS

A cytokine receptor can be used as a specific binding reagent to identify its binding partner, by taking advantage of its specificity of binding, much like an antibody would be used. The binding receptor may be a heterodimer of receptor subunits; or may involve, e.g., a complex of the DCRS with another subunit. A binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods.

The binding composition is used to screen an expression library made from a cell line which expresses a binding partner, i.e., ligand, preferably membrane associated. Standard staining techniques are used to detect or sort surface expressed ligand, or surface expressing transformed cells are screened by panning. Screening of intracellular expression is performed by various staining or immunofluorescence procedures. See also McMahan, et al. (1991) EMBO J. 10:2821-2832.

For example, on day 0, precoat 2-chamber permanox slides with 1 ml per chamber of fibronectin, 10 ng/ml in PBS, for 30 min at room temperature. Rinse once with PBS. Then plate COS cells at $2-3 \times 10^5$ cells per chamber in 1.5 ml of growth media. Incubate overnight at 37°C.

On day 1 for each sample, prepare 0.5 ml of a solution of 66 µg/ml DEAE-dextran, 66 µM chloroquine, and 4 µg DNA in serum

free DME. For each set, a positive control is prepared, e.g., of DCRS-FLAG cDNA at 1 and 1/200 dilution, and a negative mock. Rinse cells with serum free DME. Add the DNA solution and incubate 5 hr at 37°C. Remove the medium and add 0.5 ml 10%
5 DMSO in DME for 2.5 min. Remove and wash once with DME. Add 1.5 ml growth medium and incubate overnight.

On day 2, change the medium. On days 3 or 4, the cells are fixed and stained. Rinse the cells twice with Hank's Buffered Saline Solution (HBSS) and fix in 4% paraformaldehyde
10 (PFA)/glucose for 5 min. Wash 3X with HBSS. The slides may be stored at -80°C after all liquid is removed. For each chamber, 0.5 ml incubations are performed as follows. Add HBSS/saponin (0.1%) with 32 µl/ml of 1 M NaN₃ for 20 min. Cells are then washed with HBSS/saponin 1X. Add appropriate DCRS or
15 DCRS/antibody complex to cells and incubate for 30 min. Wash cells twice with HBSS/saponin. If appropriate, add first antibody for 30 min. Add second antibody, e.g., Vector anti-mouse antibody, at 1/200 dilution, and incubate for 30 min. Prepare ELISA solution, e.g., Vector Elite ABC horseradish
20 peroxidase solution, and preincubate for 30 min. Use, e.g., 1 drop of solution A (avidin) and 1 drop solution B (biotin) per 2.5 ml HBSS/saponin. Wash cells twice with HBSS/saponin. Add ABC HRP solution and incubate for 30 min. Wash cells twice with HBSS, second wash for 2 min, which closes cells. Then add
25 Vector diaminobenzoic acid (DAB) for 5 to 10 min. Use 2 drops of buffer plus 4 drops DAB plus 2 drops of H₂O₂ per 5 ml of glass distilled water. Carefully remove chamber and rinse slide in water. Air dry for a few minutes, then add 1 drop of Crystal Mount and a cover slip. Bake for 5 min at 85-90°C.

30 Evaluate positive staining of pools and progressively subclone to isolation of single genes responsible for the binding.

Alternatively, receptor reagents are used to affinity purify or sort out cells expressing a putative ligand. See,
35 e.g., Sambrook, et al. or Ausubel, et al.

Another strategy is to screen for a membrane bound receptor by panning. The receptor cDNA is constructed as described.

above. Immobilization may be achieved by use of appropriate antibodies which recognize, e.g., a FLAG sequence of a DCRS fusion construct, or by use of antibodies raised against the first antibodies. Recursive cycles of selection and
5 amplification lead to enrichment of appropriate clones and eventual isolation of receptor expressing clones.

Phage expression libraries can be screened by mammalian DCRS. Appropriate label techniques, e.g., anti-FLAG antibodies, will allow specific labeling of appropriate clones.
10

All citations herein are incorporated herein by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

15 Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited by the terms of the appended claims,
20 along with the full scope of equivalents to which such claims are entitled; and the invention is not to be limited by the specific embodiments that have been presented herein by way of example.

WHAT IS CLAIMED IS:

1. A composition of matter selected from:
 - 5 a) a substantially pure or recombinant DCRS3 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 2 or 25;
 - 10 b) a substantially pure or recombinant DCRS3 polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 2 or 25;
 - c) a natural sequence DCRS3 comprising mature SEQ ID NO: 2 or 25;
 - d) a fusion polypeptide comprising DCRS3 sequence;
 - 15 e) a substantially pure or recombinant DCRS4 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 5, 28, or 31;
 - 20 f) a substantially pure or recombinant DCRS4 polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 5, 28, or 31;
 - g) a natural sequence DCRS4 comprising mature SEQ ID NO: 5, 28, or 31; or
 - 25 h) a fusion polypeptide comprising DCRS4 sequence.
2. The substantially pure or isolated antigenic DCRS3 or DCRS4 polypeptide of Claim 1, wherein said distinct nonoverlapping segments of identity:
 - 30 a) include one of at least eight amino acids;
 - b) include one of at least four amino acids and a second of at least five amino acids;
 - c) include at least three segments of at least four, five, and six amino acids, or
 - 35 d) include one of at least twelve amino acids.
3. The composition of matter of Claim 1, wherein said:
 - a) DCRS3 polypeptide:

- 5 i) comprises a mature sequence of Table 1;
ii) is an unglycosylated form of DCRS3;
iii) is from a primate, such as a human;
iv) comprises at least seventeen amino acids of SEQ
ID NO: 2 or 25;
v) exhibits at least four nonoverlapping segments of
at least seven amino acids of SEQ ID NO: 2 or 25;
vi) comprises a sequence of at least 3 amino acids on
each side across an exon boundary;
10 vii) is a natural allelic variant of DCRS3;
viii) has a length at least about 30 amino acids;
ix) exhibits at least two non-overlapping epitopes
which are specific for a primate DCRS3;
x) is glycosylated;
15 xi) has a molecular weight of at least 30 kD with
natural glycosylation;
xii) is a synthetic polypeptide;
xiii) is attached to a solid substrate;
xiv) is conjugated to another chemical moiety;
20 xv) is a 5-fold or less substitution from natural
sequence; or
xvi) is a deletion or insertion variant from a
natural sequence; or
b) DCRS4 polypeptide:
25 i) comprises a mature sequence of Table 3;
ii) is an unglycosylated form of DCRS4;
iii) is from a primate, such as a human;
iv) comprises at least seventeen amino acids of SEQ
ID NO: 5, 28, or 31;
30 v) exhibits at least four nonoverlapping segments of
at least seven amino acids of SEQ ID NO: 5, 28,
or 31;
vi) comprises a sequence of at least 3 amino acids on
each side across an exon boundary;
35 vii) is a natural allelic variant of DCRS4;
viii) has a length at least about 30 amino acids;

- ix) exhibits at least two non-overlapping epitopes which are specific for a primate DCRS4;
x) is glycosylated;
xi) has a molecular weight of at least 30 kD with
5 natural glycosylation;
xii) is a synthetic polypeptide;
xiii) is attached to a solid substrate;
xiv) is conjugated to another chemical moiety;
xv) is a 5-fold or less substitution from natural
10 sequence; or
xvi) is a deletion or insertion variant from a natural sequence.
4. A composition comprising:
- 15 a) a substantially pure DCRS3 and another cytokine receptor family member;
b) a sterile DCRS3 polypeptide of Claim 1;
c) said DCRS3 polypeptide of Claim 1 and a carrier, wherein said carrier is:
20 i) an aqueous compound, including water, saline, and/or buffer; and/or
ii) formulated for oral, rectal, nasal, topical, or parenteral administration; or
d) a substantially pure DCRS4 and another cytokine
25 receptor family member;
e) a sterile DCRS4 polypeptide of Claim 1;
f) said DCRS4 polypeptide of Claim 1 and a carrier, wherein said carrier is:
30 i) an aqueous compound, including water, saline, and/or buffer; and/or
ii) formulated for oral, rectal, nasal, topical, or parenteral administration.
5. The fusion polypeptide of Claim 1, comprising:
- 35 a) mature protein sequence of Table 1;
b) mature protein sequence of Table 1;

- c) a detection or purification tag, including a FLAG, His6, or Ig sequence; or
 - d) sequence of another cytokine receptor protein.
- 5 6. A kit comprising a polypeptide of Claim 1, and:
- a) a compartment comprising said protein or polypeptide; or
 - b) instructions for use or disposal of reagents in said kit.
- 10 7. A binding compound comprising an antigen binding site from an antibody, which specifically binds to a natural:
- A) DCRS3 polypeptide of Claim 1, wherein:
- a) said binding compound is in a container;
 - 15 b) said polypeptide is from a human;
 - c) said binding compound is an Fv, Fab, or Fab2 fragment;
 - d) said binding compound is conjugated to another chemical moiety; or
 - e) said antibody:
- 20 i) is raised against a peptide sequence of a mature polypeptide of Table 1;
 - ii) is raised against a mature DCRS3;
 - iii) is raised to a purified human DCRS3;
 - iv) is immunoselected;
 - 25 v) is a polyclonal antibody;
 - vi) binds to a denatured DCRS3;
 - vii) exhibits a Kd to antigen of at least 30 μ M;
 - viii) is attached to a solid substrate, including a bead or plastic membrane;
 - 30 ix) is in a sterile composition; or
 - x) is detectably labeled, including a radioactive or fluorescent label; or
- B) DCRS4 polypeptide of Claim 1, wherein:
- a) said binding compound is in a container;
 - 35 b) said polypeptide is from a human;
 - c) said binding compound is an Fv, Fab, or Fab2 fragment;

- d) said binding compound is conjugated to another chemical moiety; or
- e) said antibody:
- i) is raised against a peptide sequence of a mature polypeptide of Table 3;
 - ii) is raised against a mature DCRS4;
 - iii) is raised to a purified human DCRS4;
 - iv) is immunoselected;
 - v) is a polyclonal antibody;
 - vi) binds to a denatured DCRS4;
 - vii) exhibits a K_d to antigen of at least 30 μM ;
 - viii) is attached to a solid substrate, including a bead or plastic membrane;
 - ix) is in a sterile composition; or
 - x) is detectably labeled, including a radioactive or fluorescent label.

8. A kit comprising said binding compound of Claim 7, and:
- a) a compartment comprising said binding compound; or
 - b) instructions for use or disposal of reagents in said kit.

9. A method of producing an antigen:antibody complex, comprising contacting under appropriate conditions a primate:
- a) DCRS3 polypeptide with an antibody of Claim 7, thereby allowing said complex to form; or
 - b) DCRS4 polypeptide with an antibody of Claim 7, thereby allowing said complex to form.

10. The method of Claim 9, wherein:
- a) said complex is purified from other cytokine receptors;
 - b) said complex is purified from other antibody;
 - c) said contacting is with a sample comprising an interferon;
 - d) said contacting allows quantitative detection of said antigen;

- e) said contacting is with a sample comprising said antibody; or
- f) said contacting allows quantitative detection of said antibody.

5

11. A composition comprising:

- a) a sterile binding compound of Claim 7, or
- b) said binding compound of Claim 7 and a carrier, wherein said carrier is:

10

- i) an aqueous compound, including water, saline, and/or buffer; and/or
- ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

15

12. An isolated or recombinant nucleic acid encoding said:

A) DCRS3 polypeptide of Claim 1, wherein said:

- a) DCRS3 is from a human; or
- b) said nucleic acid:
 - i) encodes an antigenic peptide sequence of Table 1;
 - 20 ii) encodes a plurality of antigenic peptide sequences of Table 1;
 - iii) exhibits identity over at least thirteen nucleotides to a natural cDNA encoding said segment;
 - 25 iv) is an expression vector;
 - v) further comprises an origin of replication;
 - vi) is from a natural source;
 - vii) comprises a detectable label;
 - viii) comprises synthetic nucleotide sequence;
 - 30 ix) is less than 6 kb, preferably less than 3 kb;
 - x) is from a primate;
 - xi) comprises a natural full length coding sequence;
 - xii) is a hybridization probe for a gene encoding said DCRS3; or
 - 35 xiii) is a PCR primer, PCR product, or mutagenesis primer; or

B) DCRS4 polypeptide of Claim 1, wherein said:

- 5
- 10
- 15
- 20
- a) DCRS4 is from a human; or
 - b) said nucleic acid:
 - i) encodes an antigenic peptide sequence of Table 3;
 - ii) encodes a plurality of antigenic peptide sequences of Table 3;
 - iii) exhibits identity over at least thirteen nucleotides to a natural cDNA encoding said segment;
 - iv) is an expression vector;
 - v) further comprises an origin of replication;
 - vi) is from a natural source;
 - vii) comprises a detectable label;
 - viii) comprises synthetic nucleotide sequence;
 - ix) is less than 6 kb, preferably less than 3 kb;
 - x) is from a primate;
 - xi) comprises a natural full length coding sequence;
 - xii) is a hybridization probe for a gene encoding said DCRS4; or
 - xiii) is a PCR primer, PCR product, or mutagenesis primer.

13. A cell or tissue comprising said recombinant nucleic acid of Claim 12.

25 14. The cell of Claim 13, wherein said cell is:

- 30
- a) a prokaryotic cell;
 - b) a eukaryotic cell;
 - c) a bacterial cell;
 - d) a yeast cell;
 - e) an insect cell;
 - f) a mammalian cell;
 - g) a mouse cell;
 - h) a primate cell; or
 - i) a human cell.

35

15. A kit comprising said nucleic acid of Claim 12, and:

- a) a compartment comprising said nucleic acid;

- b) a compartment further comprising a primate DCRS3 or DCRS4 polypeptide; or
- c) instructions for use or disposal of reagents in said kit.

5

16. A nucleic acid which:

- a) hybridizes under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 1 or 24; or
- 10 b) exhibits identity over a stretch of at least about 30 nucleotides to a primate DCRS3;
- a) hybridizes under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 4, 27, or 30; or
- 15 b) exhibits identity over a stretch of at least about 30 nucleotides to a primate DCRS4.

17. The nucleic acid of Claim 16, wherein:

- a) said wash conditions are at 45° C and/or 500 mM salt;
- 20 or
- b) said stretch is at least 55 nucleotides.

18. The nucleic acid of Claim 16, wherein:

- a) said wash conditions are at 55° C and/or 150 mM salt;
- 25 or
- b) said stretch is at least 75 nucleotides.

19. A method of modulating physiology or development of a cell or tissue culture cells comprising contacting said cell
30 with an agonist or antagonist of a mammalian DCRS3 or DCRS4.

20. The method of Claim 19, wherein said cell is transformed with a nucleic acid encoding a DCRS3 or DCRS4 and another cytokine receptor subunit.

35

SEQUENCE LISTING

<110> Schering Corporation

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01086K PCT

<140>

<141>

<150> US 09/443,060

<151> 1999-11-18

<160> 32

<170> PatentIn Ver. 2.0

<210> 1

<211> 1707

<212> DNA

<213> primate; surmised Homo sapiens

<220>

<221> CDS

<222> (1)..(1704)

<220>

<221> mat_peptide

<222> (61)..(1704)

<400> 1

atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga	48
Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly	
-20 -15 -10 -5	
gcc ctc gag ggg atg gag agg aag ctc tgc agt ccc aag cca ccc ccc	96
Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro	
-1 1 5 10	
acc aag gcc tct ctc ccc act gac cct cca ggc tgg ggc tgc ccc gac	144
Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp	
15 20 25	
ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc atc ctg gaa	192
Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu	
30 35 40	
atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg ata ctt tct	240
Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser	
45 50 55 60	
aat aat act ggg tgc tat atc aag gac aga aca ctg gac ctc agg caa	288
Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln	
65 70 75	

2

gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc cac	336
Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His	
80 85 90	
agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg gat	384
Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp	
95 100 105	
gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca gac	432
Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp	
110 115 120	
cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct gag	480
Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu	
125 130 135 140	
agc aga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc	528
Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala	
145 150 155	
ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac	576
Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn	
160 165 170	
cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg	624
Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val	
175 180 185	
gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg	672
Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser	
190 195 200	
agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac	720
Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr	
205 210 215 220	
cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag	768
Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln	
225 230 235	
tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc	816
Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu	
240 245 250	
ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat	864
Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His	
255 260 265	
cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag	912
Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu	
270 275 280	
cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa	960
Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys	
285 290 295 300	
tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg	1008

3

Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp	
305 310 315	
agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cca	1056
Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro	
320 325 330	
cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca	1104
Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala	
335 340 345	
gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca	1152
Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr	
350 355 360	
gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat cgg cca	1200
Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro	
365 370 375 380	
tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg	1248
Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly	
385 390 395	
cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg	1296
Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu	
400 405 410	
gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc	1344
Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu	
415 420 425	
ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc	1392
Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly	
430 435 440	
agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag	1440
Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys	
445 450 455 460	
cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt	1488
Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly	
465 470 475	
ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg	1536
Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu	
480 485 490	
gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac	1584
Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp	
495 500 505	
tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga	1632
Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly	
510 515 520	
ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt	1680
Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu	

4

525

530

535

540

tcg agc cct gga ccc cag gcc agc taa
 Ser Ser Pro Gly Pro Gln Ala Ser

1707

545

<210> 2

<211> 568

<212> PRT

<213> primate; surmised Homo sapiens

<400> 2

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
 -20 -15 -10 -5

Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro
 -1 1 5 10

Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp
 15 20 25

Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu
 30 35 40

Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser
 45 50 55 60

Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln
 65 70 75

Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His
 80 85 90

Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp
 95 100 105

Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp
 110 115 120

Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu
 125 130 135 140

Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala
 145 150 155

Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn
 160 165 170

Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val
 175 180 185

Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser
 190 195 200

Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr
 205 210 215 220

Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln
 225 230 235
 Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu
 240 245 250
 Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His
 255 260 265
 Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu
 270 275 280
 Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys
 285 290 295 300
 Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp
 305 310 315
 Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro
 320 325 330
 Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala
 335 340 345
 Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr
 350 355 360
 Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 365 370 375 380
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly
 385 390 395
 Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu
 400 405 410
 Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu
 415 420 425
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly
 430 435 440
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys
 445 450 455 460
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly
 465 470 475
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu
 480 485 490
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp
 495 500 505
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly
 510 515 520

Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu
 525 530 535 540

Ser Ser Pro Gly Pro Gln Ala Ser
 545

<210> 3

<211> 1704

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:reverse
 translation

<220>

<221> misc_feature

<222> (6)..(1704)

<223> n may be a, c, g, or t

<400> 3

atgccnmngng gntgggcngc nccnytnytn ytnytnytny tncarggngc nytngarggn 60
 atggarmgna arytnntyws nccnaarccn ccnccnacna argcnwsnyt nccnacngay 120
 ccnccnggnt gggngtgycc ngayytnngtn tgytayacng aytayytnc racngtnath 180
 tgyathytng aratgtggaa yytncaayccn wsnacnytna cnytnacntg gathytnwsn 240
 aayaayacng gntgytayat haargaymgn acnytngayy tnmgncarga ycartaygar 300
 garytnaarg aygargcnac nwsntgywsn ytncaymgnw sngncayaa ygcnacncay 360
 gcnacntaya cntgyccayt ggaygtntty cayttyatgg cngaygayat httywsngtn 420
 aayathacng aycarwsngg naaytaywsn cargartgyg gnwsnttyyt nytngcngar 480
 wsnmgncart ayaayathws ntggmgnwsn gaytaygarg ayccngcntt ytayatgytn 540
 aarggnaary tncartayga rytncartay mgnaaymgng gngayccntg ggcngtnwsn 600
 ccnmgnmgna arytnathws ngtngaywsn mgnwsngtnw snytnytncc nytngartty 660
 mgnaargayw snwsntayga rytncargtn mgngcnggnc cnatgccngg nwsnwsntay 720
 carggnacnt ggwsngartg gwsngayccn gtnathhttyc aracncarws ngargarytn 780
 aargarggnt ggaayccnca yytnytnytn ytnytnytny tngtnathgt nttyathccn 840
 gcnttytggw snytnaarac ncayccnytn tggmgnytnt ggaaraarat htgggcngtn 900
 ccnwsnccng armgnttytt yatgccnytn tayaarggnt gywsnggnga yttyaaraar 960
 tgggtnggng cncnttyac nggnwsnwsn ytngarytn gncntggws nccngargtn 1020

ccnwsnacny tngargtnta ywsntgy cay ccncncmgnw snccngcnaa rmgnytncar 1080
ytnacngary tncargarcc ngcngarytn gtngarwsng ayggngtncc naarcnwsn 1140
ttytggccna cngcncaraa ywsngggngn wsngcntayw sngargarmg ngaymgnccn 1200
tayggnytnng tnwsnathga yacngtnacn gtnytngayg cngarggncc ntgyacntgg 1260
ccntgywsnt gygargayga yggntayccn gcnytngayy tngaygcngg nytngarccn 1320
wsnccnggny tngargaycc nytnytngay gcnggnacna cngtnytnws ntgyggntgy 1380
gtnwsngcng gnwsnccngg nytnggnggn ccnytnngnw snytnytnga ymgnytnaar 1440
ccncnytnng cngayggnga rgaytgggcn ggnggnytn cngtggggngg nmgnwsnccn 1500
ggnggngtnw sngarwsnga rgcnggnwsn ccnytnngcng gnytngayat ggayacntty 1560
gaywsnggnt tygtnggnws ngaytgywsn wsncngtnng artgygaytt yacnwsnccn 1620
ggngaygarg gncncncmng nwsntayytn mgncartggg tngtnathcc nccncnytn 1680
wsnwsnccng gncncargc nwsn 1704

<210> 4
<211> 750
<212> DNA
<213> primate; surmised Homo sapiens

<220>
<221> CDS
<222> (1)..(747)

<220>
<221> mat_peptide
<222> (64)..(747)

<400> 4
atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt 48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
-20 -15 -10
act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
-5 -1 1 5 10
agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
15 20 25
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
30 35 40
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

8

45	50	55	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag			288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln			
60	65	70	75
gaa cct tat tac ggg agg agg ggc aaa aat aaa aat aaa ggg aat cct			336
Glu Pro Tyr Tyr Gly Arg Arg Gly Lys Asn Lys Asn Lys Gly Asn Pro			
	80	85	90
tgg ggg cca aaa caa agt aaa cgg aaa tca aag ggg aac cag aag acc			384
Trp Gly Pro Lys Gln Ser Lys Arg Lys Ser Lys Gly Asn Gln Lys Thr			
	95	100	105
aac aca gtg act gcc cca gct gcc ctg aag gca ttt gct gga tgt gca			432
Asn Thr Val Thr Ala Pro Ala Leu Lys Ala Phe Ala Gly Cys Ala			
	110	115	120
aaa ata gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg			480
Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu			
	125	130	135
ttg gta att ctc cat gct cca aat tta cca tat aga tac caa aag gaa			528
Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu			
	140	145	150
aaa aat gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt			576
Lys Asn Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe			
	160	165	170
ata att aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct			624
Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala			
	175	180	185
cac aga gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt			672
His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys			
	190	195	200
gta gtg gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga			720
Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg			
	205	210	215
agt gaa gag aga tgt gtg gaa att cca tga			750
Ser Glu Glu Arg Cys Val Glu Ile Pro			
220	225		

<210> 5

<211> 249

<212> PRT

<213> primate; surmised Homo sapiens

<400> 5

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu

-20

-15

-10

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln

9

-5 -1 1 5 10
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 15 20 25
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 30 35 40
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 45 50 55
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 60 65 70 75
 Glu Pro Tyr Tyr Gly Arg Arg Gly Lys Asn Lys Asn Lys Gly Asn Pro
 80 85 90
 Trp Gly Pro Lys Gln Ser Lys Arg Lys Ser Lys Gly Asn Gln Lys Thr
 95 100 105
 Asn Thr Val Thr Ala Pro Ala Ala Leu Lys Ala Phe Ala Gly Cys Ala
 110 115 120
 Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu
 125 130 135
 Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu
 140 145 150 155
 Lys Asn Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe
 160 165 170
 Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala
 175 180 185
 His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys
 190 195 200
 Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg
 205 210 215
 Ser Glu Glu Arg Cys Val Glu Ile Pro
 220 225

<210> 6

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence: reverse
 translation

<220>

<221> misc_feature

<222> (1)..(747)

10

<223> n may be a, c, g, or t

<400> 6

atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac ngngntngcn 60
 ggnacncarw snacncayga rwsnytnaar ccncarmng tncarttyca rwsnmgnaay 120
 ttycayaaya thytncartg gcarccnggn mgngcnytna cnggnaayws nwsngntay 180
 ttygtncart ayaarathta yggncarmgn cartggaara ayaargarga ytgytggggn 240
 acncargary tnwsntgyga yytnacnwsn garacnwsng ayathcarga rccntaytay 300
 ggnmgngmgng gnaaraayaa raayaarggn aayccntggg gncnnaarca rwsnaarmgn 360
 aarwsnaarg gnaaycaraa racnaayacn gtnacngcnc cngcngcnyt naargcntty 420
 gcnggntgyg cnaarathga yccnccngtn atgaayatha cncargtnaa yggnwsnytn 480
 ytngtnathy tncaygcnc naayytncn taymgntayc araargaraa raaygtwnsn 540
 athgargayt aytaygaryt nyntaymgn gtnttyatha thaayaayws nyngaraar 600
 garcaraarg tntaygargg ngcncaymgn gcngtngara thgargcnyt nacnccncay 660
 wsnwsntayt gygtngtngc ngarathtay carccnatgy tngaymgngm nwsncarmgn 720
 wsnrgargarm gntgygtnga rathccn 747

<210> 7

<211> 210

<212> PRT

<213> primate

<400> 7

Val	Asn	Gly	Thr	Ser	Gln	Phe	Thr	Cys	Phe	Tyr	Asn	Ser	Arg	Ala	Asn
1				5				10						15	
Ile	Ser	Cys	Val	Trp	Ser	Gln	Asp	Gly	Ala	Leu	Gln	Asp	Thr	Ser	Cys
			20					25					30		
Gln	Val	His	Ala	Trp	Pro	Asp	Arg	Arg	Arg	Trp	Asn	Gln	Thr	Cys	Glu
		35					40					45			
Leu	Leu	Pro	Val	Ser	Gln	Ala	Ser	Trp	Ala	Cys	Asn	Leu	Ile	Leu	Gly
	50					55					60				
Ala	Pro	Asp	Ser	Gln	Lys	Leu	Thr	Thr	Val	Asp	Ile	Val	Thr	Leu	Arg
65					70					75				80	
Val	Leu	Cys	Arg	Glu	Gly	Val	Arg	Trp	Arg	Val	Met	Ala	Ile	Gln	Asp
				85					90					95	
Phe	Lys	Pro	Phe	Glu	Asn	Leu	Arg	Leu	Met	Ala	Pro	Ile	Ser	Leu	Gln
				100				105						110	

11

Val Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser
 115 120 125

Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr
 130 135 140

Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys
 145 150 155 160

Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln
 165 170 175

Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr
 180 185 190

Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala
 195 200 205

Leu Gly
 210

<210> 8

<211> 231

<212> PRT

<213> primate

<400> 8

Ile Cys Ile Cys Thr Cys Val Cys Leu Gly Val Ser Val Thr Gly Glu
 1 5 10 15

Gly Gln Gly Pro Arg Ser Arg Thr Phe Thr Cys Leu Thr Asn Asn Ile
 20 25 30

Leu Arg Ile Asp Cys His Trp Ser Ala Pro Glu Leu Gly Gln Gly Ser
 35 40 45

Ser Pro Trp Leu Leu Phe Thr Ser Asn Gln Ala Pro Gly Gly Thr His
 50 55 60

Lys Cys Ile Leu Arg Gly Ser Glu Cys Thr Val Val Leu Pro Pro Glu
 65 70 75 80

Ala Val Leu Val Pro Ser Asp Asn Phe Thr Ile Thr Phe His His Cys
 85 90 95

Met Ser Gly Arg Glu Gln Val Ser Leu Val Asp Pro Glu Tyr Leu Pro
 100 105 110

Arg Arg His Val Lys Leu Asp Pro Pro Ser Asp Leu Gln Ser Asn Ile
 115 120 125

Ser Ser Gly His Cys Ile Leu Thr Trp Ser Ile Ser Pro Ala Leu Glu
 130 135 140

Pro Met Thr Thr Leu Leu Ser Tyr Glu Leu Ala Phe Lys Lys Gln Glu
 145 150 155 160

12

Glu Ala Trp Glu Gln Ala Gln His Arg Asp His Ile Val Gly Val Thr
 165 170 175

Trp Leu Ile Leu Glu Ala Phe Glu Leu Asp Pro Gly Phe Ile His Glu
 180 185 190

Ala Arg Leu Arg Val Gln Met Ala Thr Leu Glu Asp Asp Val Val Glu
 195 200 205

Glu Glu Arg Tyr Thr Gly Gln Trp Ser Glu Trp Ser Gln Pro Val Cys
 210 215 220

Phe Gln Ala Pro Gln Arg Gln
 225 230

<210> 9

<211> 216

<212> PRT

<213> primate

<400> 9

Ile Cys Ile Cys Thr Cys Val Cys Leu Gly Val Ser Val Thr Gly Glu
 1 5 10 15

Gly Gln Gly Pro Arg Ser Arg Thr Phe Thr Cys Leu Thr Asn Asn Ile
 20 25 30

Leu Arg Ile Asp Cys His Trp Ser Ala Pro Glu Leu Gly Gln Gly Thr
 35 40 45

Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
 50 55 60

Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
 65 70 75 80

Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
 85 90 95

Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
 100 105 110

Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
 115 120 125

Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
 130 135 140

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
 145 150 155 160

Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
 165 170 175

Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu

13

180	185	190
Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp		
195	200	205
Gly Ser Asn Thr Ser Lys Glu Asn		
210	215	
<210> 10		
<211> 257		
<212> PRT		
<213> primate		
<400> 10		
Leu Leu Ala Ser Asp Ser Glu Pro Leu Lys Cys Phe Ser Arg Thr Phe		
1	5	10 15
Glu Asp Leu Thr Cys Phe Trp Asp Glu Glu Glu Ala Ala Pro Ser Gly		
20	25	30
Thr Tyr Gln Leu Leu Tyr Ala Tyr Pro Arg Glu Lys Pro Arg Ala Cys		
35	40	45
Pro Leu Ser Ser Gln Ser Met Pro His Phe Gly Thr Arg Tyr Val Cys		
50	55	60
Gln Phe Pro Asp Gln Glu Glu Val Arg Leu Phe Phe Pro Leu His Leu		
65	70	75 80
Trp Val Lys Asn Val Phe Leu Asn Gln Thr Arg Thr Gln Arg Val Leu		
85	90	95
Phe Val Asp Ser Val Gly Leu Pro Ala Pro Pro Ser Ile Ile Lys Ala		
100	105	110
Met Gly Gly Ser Gln Pro Gly Glu Leu Gln Ile Ser Trp Glu Glu Pro		
115	120	125
Ala Pro Glu Ile Ser Asp Phe Leu Arg Tyr Glu Leu Arg Tyr Gly Pro		
130	135	140
Arg Asp Pro Lys Asn Ser Thr Gly Pro Thr Val Ile Gln Leu Ile Ala		
145	150	155 160
Thr Glu Thr Cys Cys Pro Ala Leu Gln Arg Pro His Ser Ala Ser Ala		
165	170	175
Leu Asp Gln Ser Pro Cys Ala Gln Pro Thr Met Pro Trp Gln Asp Gly		
180	185	190
Pro Lys Gln Thr Ser Pro Ser Arg Glu Ala Ser Ala Leu Thr Ala Glu		
195	200	205
Gly Gly Ser Cys Leu Ile Ser Gly Leu Gln Pro Gly Asn Ser Tyr Trp		
210	215	220

14

Leu Gln Leu Arg Ser Glu Pro Asp Gly Ile Ser Leu Gly Gly Ser Trp
 225 230 235 240

Gly Ser Trp Ser Leu Pro Val Thr Val Asp Leu Pro Gly Asp Ala Val
 245 250 255

Ala

<210> 11

<211> 217

<212> PRT

<213> primate

<400> 11

Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp Ala
 1 5 10 15

Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val Asn
 20 25 30

Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val Asn
 35 40 45

Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val Lys
 50 55 60

Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr Lys
 65 70 75 80

Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly Glu
 85 90 95

Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys Pro
 100 105 110

Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn Asp
 115 120 125

Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val Lys
 130 135 140

Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn Lys
 145 150 155 160

Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln Arg
 165 170 175

Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile Pro
 180 185 190

Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr Tyr
 195 200 205

Phe Arg Thr Pro Glu Ile Asn Asn Ser
 210 215

15

<210> 12
 <211> 196
 <212> PRT
 <213> primate

<400> 12
 Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile Leu Gln
 1 5 10 15

 Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe Thr Ala Gln
 20 25 30

 Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn Thr Thr Leu
 35 40 45

 Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp His Thr Leu
 50 55 60

 Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val Asn Ile
 65 70 75 80

 Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly Met Gln
 85 90 95

 Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala Pro Lys
 100 105 110

 Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Asn Ser
 115 120 125

 Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu Lys Phe
 130 135 140

 Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu Glu Pro
 145 150 155 160

 Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro Asp Arg Asn
 165 170 175

 Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr His Asp
 180 185 190

 Glu Thr Val Pro
 195

<210> 13
 <211> 196
 <212> PRT
 <213> rodent

<400> 13
 Pro Glu Lys Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile Leu Gln
 1 5 10 15

16

Trp Glu Val Pro Ala Phe Pro Lys Thr Asn Leu Thr Phe Thr Ala Gln
 20 25 30
 Tyr Glu Ser Tyr Arg Ser Phe Gln Asp His Cys Lys Arg Thr Ala Ser
 35 40 45
 Thr Gln Cys Asp Phe Ser His Leu Ser Lys Tyr Gly Asp Tyr Thr Val
 50 55 60
 Arg Val Arg Ala Glu Leu Ala Asp Glu His Ser Glu Trp Val Asn Val
 65 70 75 80
 Thr Phe Cys Pro Val Glu Asp Thr Ile Ile Gly Pro Pro Glu Met Gln
 85 90 95
 Ile Glu Ser Leu Ala Glu Ser Leu His Leu Arg Phe Ser Ala Pro Gln
 100 105 110
 Ile Glu Asn Glu Pro Glu Thr Trp Thr Leu Lys Asn Ile Tyr Asp Ser
 115 120 125
 Trp Ala Tyr Arg Val Gln Tyr Trp Lys Asn Gly Thr Asn Glu Lys Phe
 130 135 140
 Gln Val Val Ser Pro Tyr Asp Ser Glu Val Leu Arg Asn Leu Glu Pro
 145 150 155 160
 Trp Thr Thr Tyr Cys Ile Gln Val Gln Gly Phe Leu Leu Asp Gln Asn
 165 170 175
 Arg Thr Gly Glu Trp Ser Glu Pro Ile Cys Glu Arg Thr Gly Asn Asp
 180 185 190
 Glu Ile Thr Pro
 195

<210> 14
 <211> 199
 <212> PRT
 <213> primate

<400> 14
 Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
 1 5 10 15
 Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
 20 25 30
 Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
 35 40 45
 Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
 50 55 60
 Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
 65 70 75 80

17

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
85 90 95

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
100 105 110

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
115 120 125

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
130 135 140

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
145 150 155 160

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
165 170 175

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
180 185 190

Val Glu Asn Glu Leu Pro Pro
195

<210> 15

<211> 200

<212> PRT

<213> rodent

<400> 15

Pro Glu Asn Ile Asp Val Tyr Ile Ile Asp Asp Asn Tyr Thr Leu Lys
1 5 10 15

Trp Ser Ser His Gly Glu Ser Met Gly Ser Val Thr Phe Ser Ala Glu
20 25 30

Tyr Arg Thr Lys Asp Glu Ala Lys Trp Leu Lys Val Pro Glu Cys Gln
35 40 45

His Thr Thr Thr Thr Lys Cys Glu Phe Ser Leu Leu Asp Thr Asn Val
50 55 60

Tyr Ile Lys Thr Gln Phe Arg Val Arg Ala Glu Glu Gly Asn Ser Thr
65 70 75 80

Ser Ser Trp Asn Glu Val Asp Pro Phe Ile Pro Phe Tyr Thr Ala His
85 90 95

Met Ser Pro Pro Glu Val Arg Leu Glu Ala Glu Asp Lys Ala Ile Leu
100 105 110

Val His Ile Ser Pro Pro Gly Gln Asp Gly Asn Met Trp Ala Leu Glu
115 120 125

Lys Pro Ser Phe Ser Tyr Thr Ile Arg Ile Trp Gln Lys Ser Ser Ser

18

130	135	140
Asp Lys Lys Thr Ile Asn Ser Thr Tyr Tyr Val Glu Lys Ile Pro Glu		
145	150	155 160
Leu Leu Pro Glu Thr Thr Tyr Cys Leu Glu Val Lys Ala Ile His Pro		
	165	170 175
Ser Leu Lys Lys His Ser Asn Tyr Ser Thr Val Gln Cys Ile Ser Thr		
	180	185 190
Thr Val Ala Asn Lys Met Pro Val		
	195	200

<210> 16
 <211> 214
 <212> PRT
 <213> primate

<400> 16
 Pro Thr Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro Ile Val Tyr
 1 5 10 15
 Trp Glu Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr Val Glu Val
 20 25 30
 Lys Asn Tyr Gly Val Lys Asn Ser Glu Trp Ile Asp Ala Cys Ile Asn
 35 40 45
 Ile Ser His His Tyr Cys Asn Ile Ser Asp His Val Gly Asp Pro Ser
 50 55 60
 Asn Ser Leu Trp Val Arg Val Lys Ala Arg Val Gly Gln Lys Glu Ser
 65 70 75 80
 Ala Tyr Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp Gly Lys Ile
 85 90 95
 Gly Pro Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln Ile Met Ile
 100 105 110
 Asp Ile Phe His Pro Ser Val Phe Val Asn Gly Asp Glu Gln Glu Val
 115 120 125
 Asp Tyr Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr Asn Val Tyr
 130 135 140
 Val Arg Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu Thr Gln Lys
 145 150 155 160
 Glu Asp Asp Cys Asp Glu Ile Gln Cys Gln Leu Ala Ile Pro Val Ser
 165 170 175
 Ser Leu Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val Leu His Val
 180 185 190

19

Trp Gly Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile Thr Ile Phe
 195 200 205

Asn Ser Ser Ile Lys Gly
 210

<210> 17
 <211> 213
 <212> PRT
 <213> rodent

<400> 17
 Pro Thr Asn Val Leu Ile Lys Ser Tyr Asn Leu Asn Pro Val Val Cys
 1 5 10 15

Trp Glu Tyr Gln Asn Met Ser Gln Thr Pro Ile Phe Thr Val Gln Val
 20 25 30

Lys Val Tyr Ser Gly Ser Trp Thr Asp Ser Cys Thr Asn Ile Ser Asp
 35 40 45

His Cys Cys Asn Ile Tyr Gly Gln Ile Met Tyr Pro Asp Val Ser Ala
 50 55 60

Trp Ala Arg Val Lys Ala Lys Val Gly Gln Lys Glu Ser Asp Tyr Ala
 65 70 75 80

Arg Ser Lys Glu Phe Leu Met Cys Leu Lys Gly Lys Val Gly Pro Pro
 85 90 95

Gly Leu Glu Ile Arg Arg Lys Lys Glu Gln Leu Ser Val Leu Val
 100 105 110

Phe His Pro Glu Val Val Val Asn Gly Glu Ser Gln Gly Thr Met Phe
 115 120 125

Gly Asp Gly Ser Thr Cys Tyr Thr Phe Asp Tyr Thr Val Tyr Val Glu
 130 135 140

His Asn Arg Ser Gly Glu Ile Leu His Thr Lys His Thr Val Glu Lys
 145 150 155 160

Glu Glu Cys Asn Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr
 165 170 175

Leu Asp Ser Arg Tyr Cys Ile Ser Val Asp Gly Ile Ser Ser Phe Trp
 180 185 190

Gln Val Arg Thr Glu Lys Ser Lys Asp Val Cys Ile Pro Pro Phe His
 195 200 205

Asp Asp Arg Lys Asp
 210

<210> 18

20

<211> 207

<212> PRT

<213> rodent

<400> 18

Pro Ser Tyr Val Trp Phe Glu Ala Arg Phe Phe Gln His Ile Leu His
 1 5 10 15

Trp Lys Pro Ile Pro Asn Gln Ser Glu Ser Thr Tyr Tyr Glu Val Ala
 20 25 30

Leu Lys Gln Tyr Gly Asn Ser Thr Trp Asn Asp Ile His Ile Cys Arg
 35 40 45

Lys Ala Gln Ala Leu Ser Cys Asp Leu Thr Thr Phe Thr Leu Asp Leu
 50 55 60

Tyr His Arg Ser Tyr Gly Tyr Arg Ala Arg Val Arg Ala Val Asp Asn
 65 70 75 80

Ser Gln Tyr Ser Asn Trp Thr Thr Thr Glu Thr Arg Phe Thr Val Asp
 85 90 95

Glu Val Ile Leu Thr Val Asp Ser Val Thr Leu Lys Ala Met Asp Gly
 100 105 110

Ile Ile Tyr Gly Thr Ile His Pro Pro Arg Pro Thr Ile Thr Pro Ala
 115 120 125

Gly Asp Glu Tyr Glu Gln Val Phe Lys Asp Leu Arg Val Tyr Lys Ile
 130 135 140

Ser Ile Arg Lys Phe Ser Glu Leu Lys Asn Ala Thr Lys Arg Val Lys
 145 150 155 160

Gln Glu Thr Phe Thr Leu Thr Val Pro Ile Gly Val Arg Lys Phe Cys
 165 170 175

Val Lys Val Leu Pro Arg Leu Glu Ser Arg Ile Asn Lys Ala Glu Trp
 180 185 190

Ser Glu Glu Gln Cys Leu Leu Ile Thr Thr Glu Gln Tyr Phe Thr
 195 200 205

<210> 19

<211> 204

<212> PRT

<213> primate

<400> 19

Pro Pro Ser Val Trp Phe Glu Ala Glu Phe Phe His His Ile Leu His
 1 5 10 15

Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala
 20 25 30

21

Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser
 35 40 45
 Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val Thr Leu Asp Leu Tyr His
 50 55 60
 Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala Val Asp Gly Ser Arg His
 65 70 75 80
 Ser Asn Trp Thr Val Thr Asn Thr Arg Phe Ser Val Asp Glu Val Thr
 85 90 95
 Leu Thr Val Gly Ser Val Asn Leu Glu Ile His Asn Gly Phe Ile Leu
 100 105 110
 Gly Lys Ile Gln Leu Pro Arg Pro Lys Met Ala Pro Ala Asn Asp Thr
 115 120 125
 Tyr Glu Ser Ile Phe Ser His Phe Arg Glu Tyr Glu Ile Ala Ile Arg
 130 135 140
 Lys Val Pro Gly Asn Phe Thr Phe Thr His Lys Lys Val Lys His Glu
 145 150 155 160
 Asn Phe Ser Leu Leu Thr Ser Gly Glu Val Gly Glu Phe Cys Val Gln
 165 170 175
 Val Lys Pro Ser Val Ala Ser Arg Ser Asn Lys Gly Met Trp Ser Lys
 180 185 190
 Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr Phe Thr
 195 200

<210> 20

<211> 208

<212> PRT

<213> primate

<400> 20

Pro Leu Asn Pro Arg Leu His Leu Tyr Asn Asp Glu Gln Ile Leu Thr
 1 5 10 15
 Trp Glu Pro Ser Pro Ser Ser Asn Asp Pro Arg Pro Val Val Tyr Gln
 20 25 30
 Val Glu Tyr Ser Phe Ile Asp Gly Ser Trp His Arg Leu Leu Glu Pro
 35 40 45
 Asn Cys Thr Asp Ile Thr Glu Thr Lys Cys Asp Leu Thr Gly Gly Gly
 50 55 60
 Arg Leu Lys Leu Phe Pro His Pro Phe Thr Val Phe Leu Arg Val Arg
 65 70 75 80
 Ala Lys Arg Gly Asn Leu Thr Ser Lys Trp Val Gly Leu Glu Pro Phe
 85 90 95

22

Gln His Tyr Glu Asn Val Thr Val Gly Pro Pro Lys Asn Ile Ser Val
100 105 110

Thr Pro Gly Lys Gly Ser Leu Val Ile His Phe Ser Pro Pro Phe Asp
115 120 125

Val Phe His Gly Ala Thr Phe Gln Tyr Leu Val His Tyr Trp Glu Lys
130 135 140

Ser Glu Thr Gln Gln Glu Gln Val Glu Gly Pro Phe Lys Ser Asn Ser
145 150 155 160

Ile Val Leu Gly Asn Leu Lys Pro Tyr Arg Val Tyr Cys Leu Gln Thr
165 170 175

Glu Ala Gln Leu Ile Leu Lys Asn Lys Lys Ile Arg Pro His Gly Leu
180 185 190

Leu Ser Asn Val Ser Cys His Glu Thr Thr Ala Asn Ala Ser Ala Arg
195 200 205

<210> 21
<211> 207
<212> PRT
<213> primate

<400> 21
Pro Ala Asn Ile Thr Phe Leu Ser Ile Asn Met Lys Asn Val Leu Gln
1 5 10 15

Trp Thr Pro Pro Glu Gly Leu Gln Gly Val Lys Val Thr Tyr Thr Val
20 25 30

Gln Tyr Phe Ile Tyr Gly Gln Lys Lys Trp Leu Asn Lys Ser Glu Cys
35 40 45

Arg Asn Ile Asn Arg Thr Tyr Cys Asp Leu Ser Ala Glu Thr Ser Asp
50 55 60

Tyr Glu His Gln Tyr Tyr Ala Lys Val Lys Ala Ile Trp Gly Thr Lys
65 70 75 80

Cys Ser Lys Trp Ala Glu Ser Gly Arg Phe Tyr Pro Phe Leu Glu Thr
85 90 95

Gln Ile Gly Pro Pro Glu Val Ala Leu Thr Thr Asp Glu Lys Ser Ile
100 105 110

Ser Val Val Leu Thr Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp
115 120 125

Leu Pro Val Ser Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val

23

130 135 140
 Ser Val Leu Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr
 145 150 155 160
 Asn His Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys
 165 170 175
 Val His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 180 185 190
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 195 200 205

 <210> 22
 <211> 234
 <212> PRT
 <213> primate

 <400> 22
 Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr
 1 5 10 15
 Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu
 20 25 30
 Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln
 35 40 45
 Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu
 50 55 60
 Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg
 65 70 75 80
 Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr
 85 90 95
 Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln
 100 105 110
 Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His
 115 120 125
 Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu
 130 135 140
 Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg
 145 150 155 160
 Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr
 165 170 175
 Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 180 185 190

24

Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe Ser
 195 200 205

Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys Tyr
 210 215 220

Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro
 225 230

<210> 23

<211> 201

<212> PRT

<213> primate

<400> 23

Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser
 1 5 10 15

Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu
 20 25 30

Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys
 35 40 45

Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser
 50 55 60

Thr His Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr
 65 70 75 80

Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser
 85 90 95

Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn
 100 105 110

Val Met Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp
 115 120 125

Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His
 130 135 140

Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile
 145 150 155 160

Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu
 165 170 175

His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu
 180 185 190

Leu Pro Pro Gly Gln Glu Ser Glu Ser
 195 200

<210> 24

<211> 1617

<212> DNA

<213> primate; surmised Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<220>

<221> mat_peptide

<222> (61)..(1614)

<220>

<221> misc_feature

<222> (1)..(1617)

<223> n may be a, c, g, or t; translated amino acid
depends on genetic code

<400> 24

atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga	48
Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly	
-20 -15 -10 -5	
ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
-1 1 5 10	
gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	
15 20 25	
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	
30 35 40	
tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc	240
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	
45 50 55 60	
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc	288
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	
65 70 75	
aac atc aca gac cag tct ggc aac tac tcc cag gan tgt ggc agc ttt	336
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Xaa Cys Gly Ser Phe	
80 85 90	
ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	
95 100 105	
acc ttc tca gga cag tat aat atn tcc tgg cgc tca gat tac gaa gac	432
Thr Phe Ser Gly Gln Tyr Asn Xaa Ser Trp Arg Ser Asp Tyr Glu Asp	
110 115 120	
cct gcc ttc tac atg ctg aaa ggc aag ctt caa tat gag ctg cag tac	480
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr	

26

125	130	135	140	
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc	528			
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile				
145	150	155		
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa	576			
Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys				
160	165	170		
gac tcg agc tat gag ctg can gtg cgg gca ggg ccc atg cct ggc tcc	624			
Asp Ser Ser Tyr Glu Leu Xaa Val Arg Ala Gly Pro Met Pro Gly Ser				
175	180	185		
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc tgt cag	672			
Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Cys Gln				
190	195	200		
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt	720			
Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu				
205	210	215	220	
ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag	768			
Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys				
225	230	235		
acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc	816			
Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser				
240	245	250		
cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc	864			
Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe				
255	260	265		
aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga	912			
Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly				
270	275	280		
ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac	960			
Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His				
285	290	295	300	
cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa	1008			
Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu				
305	310	315		
cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg	1056			
Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp				
320	325	330		
ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat	1104			
Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp				
335	340	345		
cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca	1152			
Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala				
350	355	360		

27

gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca 1200
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 365 370 375 380

gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac 1248
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 385 390 395

cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca 1296
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 400 405 410

gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga 1344
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 415 420 425

cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc 1392
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 430 435 440

tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca 1440
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 445 450 455 460

ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc 1488
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 465 470 475

tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac 1536
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
 480 485 490

gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg 1584
 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
 495 500 505

cca ctt tcg agc cct gga ccc cag gcc agc taa 1617
 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 510 515

<210> 25

<211> 538

<212> PRT

<213> primate; surmised Homo sapiens

<400> 25

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
 -20 -15 -10 -5

Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 -1 1 5 10

Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 15 20 25

28

Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 30 35 40
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 45 50 55 60
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 65 70 75
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Xaa Cys Gly Ser Phe
 80 85 90
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 95 100 105
 Thr Phe Ser Gly Gln Tyr Asn Xaa Ser Trp Arg Ser Asp Tyr Glu Asp
 110 115 120
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 125 130 135 140
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 145 150 155
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 160 165 170
 Asp Ser Ser Tyr Glu Leu Xaa Val Arg Ala Gly Pro Met Pro Gly Ser
 175 180 185
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Cys Gln
 190 195 200
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
 205 210 215 220
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 225 230 235
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
 240 245 250
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 255 260 265
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 270 275 280
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 285 290 295 300
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 305 310 315
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 320 325 330

29

Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 335 340 345

Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 350 355 360

Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 365 370 375 380

Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 385 390 395

Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 400 405 410

Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 415 420 425

Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 430 435 440

Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 445 450 455 460

Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 465 470 475

Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
 480 485 490

Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
 495 500 505

Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 510 515

<210> 26

<211> 1614

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (1)..(1614)

<223> n may be a, c, g, or t

<220>

<223> Description of Artificial Sequence:reverse
 translation

<400> 26

atgccnmngn gntgggcngc nccnytnytn ytnytnytn tncarggngg ntggggntgy 60

ccngayytng tntgytayac ngaytayytn caracngtna thtgyathyt ngaratgtgg 120

aayytncayc cnwsnacnytnacn tggcargayc artaygarga rytnaargay 180

gargcnacnw sntgywsnyt ncaymgnwsn gncayaayg cnacncaygc nactayacn 240
 tgycaatgg aygtnttyca yttyatggcn gaygayatht tywsngtnaa yathacngay 300
 carwsnggna aytaywsna rnnntgyggn wsnttyytny tngcngarws nathaarcn 360
 gncncncnt tyaygtnac ngtnacntty wsnggncart ayaaynnnws ntggmgnwsn 420
 gaytaygarg ayccngcntt ytayatgytn aarggnaary tncartayga rytncartay 480
 mgnaymgng gngayccntg ggcngtnwsn ccnmgnmgn aarytnathws ngtngaywsn 540
 mgnwsngtnw snytnytnc nytngartty mgnargayw snwsntayga rytnnngtn 600
 mgngcnggnc cnatgccngg nwsnwsntay carggnacnt ggwsngartg gwsngayccn 660
 gtnathtgyc aracncarws ngargarytn aargargnt ggaayccna yytnytnytn 720
 ytnytnytny tngtnathgt nttyathccn gcnttytgw snytnaarac ncayccnytn 780
 tggmgnytnt ggaaraarat htggcngtn ccnwsnccng armgnttytt yatgccnytn 840
 tayaargnt gywsngnga yttyaaraar tgggtnggng cncnttyac nggnwsnwsn 900
 ytngarytng gncntggws nccngargtn ccnwsnacny tngargnta ywsntgyca 960
 ccncnmgnw snccngcnaa rmgnytncar ytnacgary tncargarcc ngcngarytn 1020
 gtngarwsng ayggngtncc naarcnwsn ttytgccna cngcncaraa ywsngngggn 1080
 wsngcntayw sngargarmg ngaymgncn tayggnytn twnsnathga yacngtnacn 1140
 gtntyngayg cngarggncc ntgyacntgg cntgywsnt gygargayga yggntayccn 1200
 gcnytngayy tngaygcngg nytngarccn wsncnggny tngargaycc nytnytngay 1260
 gcnggnacna cngtnytnws ntgyggntgy gtnwsngcng gnwsnccngg nytnngnggn 1320
 ccnytnngnw snytnytna ymgnytnaar ccncnytn cngayggnga rgaytggcn 1380
 ggnggnytn cntgggngg nmgnwsnccn ggngngtnw sngarwsnga rgcnggnwsn 1440
 ccnytnccng gnytngayt ggayacntty gaywsngnt tygtnggnws ngaytgywsn 1500
 wsncngtn artgygaytt yacnwsnccn ggngaygarg gncncnmg nwsntayytn 1560
 mgncartggg tngtnathcc ncncnytn wsnwsnccng gncncargc nwsn 1614

<210> 27

<211> 696

<212> DNA

<213> primate; surmised Homo sapiens

<220>

<221> CDS

<222> (1)..(693)

<220>

<221> mat_peptide

<222> (64)..(693)

<400> 27

atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt	48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
-20 -15 -10	
act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
-5 -1 1 5 10	
agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
15 20 25	
ccc ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
30 35 40	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
45 50 55	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
60 65 70 75	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
80 85 90	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
95 100 105	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
110 115 120	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
125 130 135	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
140 145 150 155	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
160 165 170	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	

175

185

672

696

<211> 231

<212> PRT

<213> primate; surmised Homo sapiens

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
-20 -15 -10

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
-5 -1 1 5 10

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
15 20 25

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
30 35 40

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
45 50 55

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
60 65 70 75

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
80 85 90

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
95 100 105

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
110 115 120

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
125 130 135

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
140 145 150 155

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
160 165 170

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
175 180 185

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu

190	195	200
-----	-----	-----

Glu Arg Cys Val Glu Ile Pro
 205 210

<210> 29
 <211> 693
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse translation

<220>
 <221> misc_feature
 <222> (1)..(693)
 <223> n may be a, c, g, or t

<400> 29
 atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac nggngtngcn 60
 ggnacncarw snacncayga rwsnytnaar ccncarmgng tncarttyca rwsnmgnaay 120
 ttycayaaya thytncartg gcarcnngn mgngcnytnc cnggnaayws nwsngtntay 180
 ttygtncart ayaarathta yggncarmgn cartggaara ayaargarga ytggtggggg 240
 acncargary tnwsntgyga yytnacnwsn garacnwsng ayathcarga rcntaytay 300
 ggnmgngtnm gngcngcnws ngcnggnwsn taywsngart ggwsnatgac nccnmgtty 360
 acncntggt gggaracnaa rathgayccn ccngtnatga ayathacnca rgtnaayggn 420
 wsnytnytn tnathtytnca ygcncnaay ytnccntaym gntaycaraa rgaraaraay 480
 gtnwsnathg argaytayta ygarytnytn taymgngtnt tyathathaa yaaywsnytn 540
 garaargarc araargnta ygarggngcn caymgngcng tngarathga rgnytncn 600
 ccncaywsnw sntaytgygt ngtnngcngar athtaycarc cnatgytna ymgngnwsn 660
 carmgnwsng argarmgtg ygtngarath ccn 693

<210> 30
 <211> 526
 <212> DNA
 <213> primate; surmised Homo sapiens

<220>
 <221> CDS
 <222> (1)..(390)

<220>
 <221> mat_peptide

<222> (64)..(390)

<400> 30

atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttt ttc ctt 48
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu

-20

-15

-10

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln

-5

-1 1

5

10

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln

15

20

25

cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr

30

35

40

aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

45

50

55

act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln

60

65

70

75

gaa tct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca 336
 Glu Ser Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser

80

85

90

gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aga gca aaa 384
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys

95

100

105

ggg tta tgaaggggct cacagagcgg ttgaaattga agctctaaca ccacactcca 440
 Gly Leu

gctactgtgt agtggctgaa atatatcagc ccacgttaga cagaagaagt cagagaagtg 500

aagagagatg tgtggaaatt ccatga 526

<210> 31

<211> 130

<212> PRT

<213> primate; surmised Homo sapiens

<400> 31

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 -20 -15 -10

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 -5 -1 1 5 10

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 15 20 25

35

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 30 35 40

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 45 50 55

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 60 65 70 75

Glu Ser Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 80 85 90

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys
 95 100 105

Gly Leu

<210> 32

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:reverse
 translation

<220>

<221> misc_feature

<222> (1)..(390)

<223> n may be a, c, g, or t

<400> 32

atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac nggngtngcn 60
 ggnacncarw snacncayga rwsnytnaar ccncarmgng tncarttyca rwsnmgnaay 120
 ttcayaaya thytncartg gcarccnggn mgngcnytna cnggnaayws nwsngtntay 180
 ttygtncart ayaarathta yggncarmgn cartggaara ayaargarga ytgytggggg 240
 acncargary tnwsntgyga yytnacnwsn garacnwsng ayathcarga rwsntaytay 300
 ggnmgngtnm gngcngcnws ngcnggnwsn taywsngart ggwsnatgac nccnmgntty 360
 acnccntggt gggarmgngc naarggnytn 390